

SEQUENCE LISTING

<110> University of Utah Research Foundation

<120> COMPOSITIONS AND METHODS FOR MODULATING
DHR96

<130> 21101.0053P1

<140> Unassigned

<141> 2005-01-13

<150> 60/536,337

<151> 2004-01-13

<160> 60

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1543

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 1

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Phe	Gln	Asp	Leu	Lys	Leu	Lys	Arg	Arg	Lys	Ile	Asp	Ser	Arg	Cys	Ser	20	25	30	
Ser	Asp	Gly	Glu	Ser	Ile	Ala	Asp	Thr	Ser	Thr	Ser	Ser	Pro	Asp	Leu	35	40	45	
Leu	Ala	Pro	Met	Ser	Pro	Lys	Leu	Cys	Asp	Ser	Gly	Ser	Ala	Gly	Ala	50	55	60	
Ser	Leu	Gly	Ala	Ser	Leu	Pro	Leu	Pro	Leu	Ala	Leu	Pro	Leu	Pro	Met	65	70	75	80
Ala	Leu	Pro	Leu	Pro	Met	Ser	Leu	Pro	Leu	Pro	Leu	Thr	Ala	Ala	Ser	85	90	95	
Ser	Ala	Val	Thr	Val	Ser	Leu	Ala	Ala	Val	Val	Ala	Ala	Val	Ala	Glu	100	105	110	
Thr	Gly	Gly	Ala	Gly	Ala	Gly	Gly	Ala	Gly	Thr	Ala	Val	Thr	Ala	Ser	115	120	125	
Gly	Ala	Gly	Pro	Cys	Val	Ser	Thr	Ser	Ser	Thr	Thr	Ala	Ala	Ala	Ala	130	135	140	
Thr	Ser	Ser	Thr	Ser	Ser	Leu	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	145	150	155	160
Thr	Ser	Ser	Ser	Thr	Ser	Ser	Ala	Ser	Pro	Thr	Ala	Gly	Ala	Ser	Ser	165	170	175	
Thr	Ala	Thr	Cys	Pro	Ala	Ser	Ser	Ser	Ser	Ser	Ser	Gly	Asn	Gly	Ser	180	185	190	
Gly	Gly	Lys	Ser	Gly	Ser	Ile	Lys	Gln	Glu	His	Thr	Glu	Ile	His	Ser	195	200	205	
Ser	Ser	Ser	Ala	Ile	Ser	Ala	Ala	Ala	Ala	Ser	Thr	Val	Met	Ser	Pro	210	215	220	
Pro	Pro	Ala	Glu	Ala	Thr	Arg	Ser	Ser	Pro	Ala	Thr	Pro	Glu	Gly	Gly	225	230	235	240

Gly	Pro	Ala	Gly	Asp	Gly	Ser	Gly	Ala	Thr	Gly	Gly	Gly	Asn	Thr	Ser		
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Gly	Gly	Ser	Thr	Ala	Gly	Val	Ala	Ile	Asn	Glu	His	Gln	Asn	Asn	Gly		
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Asn	Gly	Ser	Gly	Gly	Ser	Ser	Arg	Ala	Ser	Pro	Asp	Ser	Leu	Glu	Glu		
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Lys	Pro	Ser	Thr	Thr	Thr	Thr	Thr	Gly	Arg	Pro	Thr	Leu	Thr	Pro	Thr		
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Asn	Gly	Val	Leu	Ser	Ser	Ala	Ser	Ala	Gly	Thr	Gly	Ile	Ser	Thr	Gly		
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Ser	Ser	Ala	Lys	Leu	Ser	Glu	Ala	Gly	Met	Ser	Val	Ile	Arg	Ser	Val		
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Lys	Glu	Glu	Arg	Leu	Leu	Asn	Val	Ser	Ser	Lys	Met	Leu	Val	Phe	His		
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Gln	Gln	Arg	Glu	Gln	Glu	Thr	Lys	Ala	Val	Ala	Ala	Ala	Ala	Ala	Ala		
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Ala	Ala	Ala	Gly	His	Val	Thr	Val	Leu	Val	Thr	Pro	Ser	Arg	Ile	Lys		
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Ser	Glu	Pro	Pro	Pro	Pro	Ala	Ser	Pro	Ser	Ser	Thr	Ser	Ser	Thr	Gln		
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Arg	Glu	Arg	Asp	Arg	Asp	Arg	Glu	Arg	Glu	Arg	Glu	Gln	Ser	Ile	Ser		
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Ser	Ser	Gln	Gln	His	Leu	Ser	Arg	Val	Ser	Ala	Ser	Pro	Pro	Thr	Gln		
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Leu	Ser	His	Gly	Ser	Leu	Gly	Pro	Asn	Ile	Val	Gln	Thr	His	His	Leu		
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Thr	Glu	His	Leu	Leu	Ser	Gln	Ser	Met	Gln	His	Leu	Thr	Gln	Gln	Gln		
			485						490					495			
Ala	Ile	His	Leu	His	His	Leu	Leu	Gly	Gln	Gln	Gln	Gln	Gln	Gln	Gln		
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Ala	Ser	His	Pro	Gln	Gln	Gln	Gln	Gln	Gln	Gln	His	Ser	Pro	His	Ser		
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Leu	Val	Arg	Val	Lys	Lys	Glu	Pro	Asn	Val	Gly	Gln	Arg	His	Leu	Ser		
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Pro	His	His	Gln	Gln	Gln	Ser	Pro	Leu	Leu	Gln	His	His	Gln	Gln	Gln		
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Gln	Gln	Gln	His	His	Gln	Gln	Gln	Pro	Gln	Ala	Leu	Ala	Leu	Met	His		
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Pro	Ala	Ser	Leu	Ala	Leu	Arg	Asn	Ser	Asn	Arg	Asp	Ala	Ala	Ile	Leu		
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Val	Ala	Ala	Gln	Arg	Met	Val	Cys	Phe	Ser	Asn	Ala	Arg	Ile	Asn	Gly		
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Val	Lys	Pro	Glu	Val	Ile	Gly	Gly	Pro	Leu	Gly	Asn	Leu	Arg	Pro	Val		
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Gly	Val	Gly	Gly	Gly	Asn	Gly	Ser	Gly	Ser	Val	Gln	Cys	Pro	Ser	Pro		
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His	Pro	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Gln	Leu	Ser	Pro	Gln	Thr	Pro		
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Ser	Gln	Thr	Pro	Pro	Arg	Gly	Thr	Pro	Thr	Val	Ile	Met	Gly	Glu	Ser		
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Cys Gly Val Arg Thr Met Val Trp Gly Tyr Glu Pro Pro Pro Pro Ser
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 Ala Gly Gln Ser His Gly Gln His Pro Gln Gln Gln Gln Gln Ser Pro
 740 745 750
 His His Gln Pro Gln Gln Gln Gln Gln Gln Gln Gln Gln Ser Gln
 755 760 765
 Gln Gln Gln Gln Gln Gln Gln Gln Ser Leu Gly Gln Gln Gln His
 770 775 780
 Cys Leu Ser Ser Pro Ser Ala Gly Ser Leu Thr Pro Ser Ser Ser Ser
 785 790 795 800
 Gly Gly Gly Ser Val Ser Gly Gly Gly Val Gly Gly Pro Leu Thr Pro
 805 810 815
 Ser Ser Val Ala Pro Gln Asn Asn Glu Glu Ala Ala Gln Leu Leu Leu
 820 825 830
 Ser Leu Gly Gln Thr Arg Ile Gln Asp Met Arg Ser Arg Pro His Pro
 835 840 845
 Phe Arg Thr Pro His Ala Leu Asn Met Glu Arg Leu Trp Ala Gly Asp
 850 855 860
 Tyr Ser Gln Leu Pro Pro Gly Gln Leu Gln Ala Leu Asn Leu Ser Ala
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 Gln Gln Gln Gln Trp Gly Ser Ser Asn Ser Thr Gly Leu Gly Gly Val
 885 890 895
 Gly Gly Gly Met Gly Gly Arg Asn Leu Glu Ala Pro His Glu Pro Thr
 900 905 910
 Asp Glu Asp Glu Gln Pro Leu Val Cys Met Ile Cys Glu Asp Lys Ala
 915 920 925
 Thr Gly Leu His Tyr Gly Ile Ile Thr Cys Glu Gly Cys Lys Gly Phe
 930 935 940
 Phe Lys Arg Thr Val Gln Asn Arg Arg Val Tyr Thr Cys Val Ala Asp
 945 950 955 960
 Gly Thr Cys Glu Ile Thr Lys Ala Gln Arg Asn Arg Cys Gln Tyr Cys
 965 970 975
 Arg Phe Lys Lys Cys Ile Glu Gln Gly Met Val Leu Gln Ala Val Arg
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 Glu Asp Arg Met Pro Gly Gly Arg Asn Ser Gly Ala Val Tyr Asn Leu
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 Tyr Lys Val Lys Tyr Lys Lys His Lys Lys Thr Asn Gln Lys Gln Gln
 1010 1015 1020
 Gln Gln Ala Ala Gln Gln Gln Gln Gln Ala Ala Ala Gln Gln Gln
 1025 1030 1035 1040
 His Gln Gln Gln Gln Gln His Gln Gln His Gln Gln His Gln Gln Gln
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 Gln Leu His Ser Pro Leu His His His His His Gln Gly His Gln Ser
 1060 1065 1070
 His His Ala Gln Gln Gln His His Pro Gln Leu Ser Pro His His Leu
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 Leu Ser Pro Gln Gln Gln Gln Leu Ala Ala Ala Val Ala Ala Ala Ala
 1090 1095 1100
 Gln His Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Ala
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 Lys Leu Met Gly Gly Val Val Asp Met Lys Pro Met Phe Leu Gly Pro
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 Ala Leu Lys Pro Glu Leu Leu Gln Ala Pro Pro Met His Ser Pro Ala
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 Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Ala Ser
 1155 1160 1165
 Pro His Leu Ser Leu Ser Ser Pro His Gln Gln Gln Gln Gln Gln Gln
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 1185 1190 1195 1200

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<210> 3

<211> 803

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 3

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 20             25             30
Pro Ser Ser Pro Ala Leu Ala Ala Gly Gly Asn Ser Ser Asn Asn Ala
 35             40             45
Ala Ser Gly Ser Asn Asn Asn Ser Ala Ser Gly Asn Asn Thr Ser Ser
 50             55             60
Ser Ser Asn Asn Asn Asn Asn Asn Asn Asp Asn Asp Ala His Val
 65             70             75             80
Leu Thr Lys Phe Glu His Glu Tyr Asn Ala Tyr Thr Leu Gln Leu Ala
 85             90             95
Gly Gly Gly Gly Ser Gly Ser Gly Asn Gln Gln His His Ser Asn His
100            105            110
Ser Asn His Gly Asn His His Gln Gln Gln Gln Gln Gln Gln Gln
115            120            125
Gln Gln Gln His Gln Gln Gln Gln Gln Glu His Tyr Gln Gln Gln Gln
130            135            140
Gln Gln Asn Ile Ala Asn Asn Ala Asn Gln Phe Asn Ser Ser Ser Tyr
145            150            155            160
Ser Tyr Ile Tyr Asn Phe Asp Ser Gln Tyr Ile Phe Pro Thr Gly Tyr
165            170            175
Gln Asp Thr Thr Ser Ser His Ser Gln Gln Ser Gly Gly Gly Gly Gly
180            185            190
Gly Gly Gly Gly Asn Leu Leu Asn Gly Ser Ser Gly Gly Ser Ser Ala
195            200            205
Gly Gly Gly Tyr Met Leu Leu Pro Gln Ala Ala Ser Ser Ser Gly Asn
210            215            220
Asn Gly Asn Pro Asn Ala Gly His Met Ser Ser Gly Ser Val Gly Asn
225            230            235            240
Gly Ser Gly Gly Ala Gly Asn Gly Gly Ala Gly Gly Asn Ser Gly Pro
245            250            255
Gly Asn Pro Met Gly Gly Thr Ser Ala Thr Pro Gly His Gly Gly Glu
260            265            270
Val Ile Asp Phe Lys His Leu Phe Glu Glu Leu Cys Pro Val Cys Gly
275            280            285
Asp Lys Val Ser Gly Tyr His Tyr Gly Leu Leu Thr Cys Glu Ser Cys
290            295            300

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Lys Gly Phe Phe Lys Arg Thr Val Gln Asn Lys Lys Val Tyr Thr Cys
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 Val Ala Glu Arg Ser Cys His Ile Asp Lys Thr Gln Arg Lys Arg Cys
 325 330 335
 Pro Tyr Cys Arg Phe Gln Lys Cys Leu Glu Val Gly Met Lys Leu Glu
 340 345 350
 Ala Val Arg Ala Asp Arg Met Arg Gly Gly Arg Asn Lys Phe Gly Pro
 355 360 365
 Met Tyr Lys Arg Asp Arg Ala Arg Lys Leu Gln Val Met Arg Gln Arg
 370 375 380
 Gln Leu Ala Leu Gln Ala Leu Arg Asn Ser Met Gly Pro Asp Ile Lys
 385 390 395 400
 Pro Thr Pro Ile Ser Pro Gly Tyr Gln Gln Ala Tyr Pro Asn Met Asn
 405 410 415
 Ile Lys Gln Glu Ile Gln Ile Pro Gln Val Ser Ser Leu Thr Gln Ser
 420 425 430
 Pro Asp Ser Ser Pro Ser Pro Ile Ala Ile Ala Leu Gly Gln Val Asn
 435 440 445
 Ala Ser Thr Gly Gly Val Ile Ala Thr Pro Met Asn Ala Gly Thr Gly
 450 455 460
 Gly Ser Gly Gly Gly Gly Leu Asn Gly Pro Ser Ser Val Gly Asn Gly
 465 470 475 480
 Asn Ser Ser Asn Gly Ser Ser Asn Gly Asn Asn Asn Ser Ser Thr Gly
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 Asn Gly Thr Ser Gly Gly Gly Gly Gly Asn Asn Ala Gly Gly Gly Gly
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 Gly Gly Thr Asn Ser Asn Asp Gly Leu His Arg Asn Gly Gly Asn Gly
 515 520 525
 Asn Ser Ser Cys His Glu Ala Gly Ile Gly Ser Leu Gln Asn Thr Ala
 530 535 540
 Asp Ser Lys Leu Cys Phe Asp Ser Gly Thr His Pro Ser Ser Thr Ala
 545 550 555 560
 Asp Ala Leu Ile Glu Pro Leu Arg Val Ser Pro Met Ile Arg Glu Phe
 565 570 575
 Val Gln Ser Ile Asp Asp Arg Glu Trp Gln Thr Gln Leu Phe Ala Leu
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 Arg Asn Thr Val Phe Phe Lys Asp Leu Lys Val Asp Asp Gln Met Lys
 625 630 635 640
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 His Arg Ile His Asn Gly Leu Pro Asp Glu Thr Gln Leu Asn Asn Gly
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 675 680 685
 Gly Asp Tyr Phe Asn Glu Leu Gln Asn Lys Leu Gln Asp Leu Lys Phe
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 Asn Val Gln Ala Ala Leu Leu Asp Tyr Thr Leu Thr Cys Tyr Pro Ser
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Gly Ser Ala Pro Thr Gln Thr Leu Leu Met Glu Met Leu His Ala Lys
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<210> 4

<211> 3269

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
 synthetic construct

<400> 4

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cccgcagggc	taccaggaca	ccacctcctc	acactcgcaa	cagagcggag	gaggcgggtg	600
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<210> 5

<211> 487

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 5

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Ala Gly Gln Asn Asn Ser Ser Gly Ser Ile Lys Ala Gln Ile Glu Ile
 35          40          45
Ile Pro Cys Lys Val Cys Gly Asp Lys Ser Ser Gly Val His Tyr Gly
 50          55          60
Val Ile Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Gln Ser
 65          70          75          80
Ser Val Val Asn Tyr Gln Cys Pro Arg Asn Lys Gln Cys Val Val Asp
 85          90          95
Arg Val Asn Arg Asn Arg Cys Gln Tyr Cys Arg Leu Gln Lys Cys Leu
 100         105         110
Lys Leu Gly Met Ser Arg Asp Ala Val Lys Phe Gly Arg Met Ser Lys
 115         120         125
Lys Gln Arg Glu Lys Val Glu Asp Glu Val Arg Phe His Arg Ala Gln
 130         135         140
Met Arg Ala Gln Ser Asp Ala Ala Pro Asp Ser Ser Val Tyr Asp Thr
 145         150         155         160
Gln Thr Pro Ser Ser Ser Asp Gln Leu His His Asn Asn Tyr Asn Ser
 165         170         175
Tyr Ser Gly Gly Tyr Ser Asn Asn Glu Val Gly Tyr Gly Ser Pro Tyr
 180         185         190
Gly Tyr Ser Ala Ser Val Thr Pro Gln Gln Thr Met Gln Tyr Asp Ile
 195         200         205
Ser Ala Asp Tyr Val Asp Ser Thr Thr Tyr Glu Pro Arg Ser Thr Ile
 210         215         220
Ile Asp Pro Glu Phe Ile Ser His Ala Asp Gly Asp Ile Asn Asp Val
 225         230         235         240
Leu Ile Lys Thr Leu Ala Glu Ala His Ala Asn Thr Asn Thr Lys Leu
 245         250         255
Glu Ala Val His Asp Met Phe Arg Lys Gln Pro Asp Val Ser Arg Ile
 260         265         270
Leu Tyr Tyr Lys Asn Leu Gly Gln Glu Glu Leu Trp Leu Asp Cys Ala
 275         280         285
Glu Lys Leu Thr Gln Met Ile Gln Asn Ile Ile Glu Phe Ala Lys Leu
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Ile Pro Gly Phe Met Arg Leu Ser Gln Asp Asp Gln Ile Leu Leu Leu
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<210> 7

<211> 723

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 7

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          20          25          30
Arg Asn Ala Leu Ala Lys Lys Gln Phe Thr Cys Pro Phe Asn Gln Asn
      35           40           45

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65					70					75					80
Glu	Asp	Lys	Leu	Ile	Lys	Arg	Arg	Lys	Ile	Glu	Thr	Asn	Arg	Ala	Lys
				85					90					95	
Arg	Arg	Leu	Met	Glu	Asn	Gly	Thr	Asp	Ala	Cys	Asp	Ala	Asp	Gly	Gly
			100					105					110		
Glu	Glu	Arg	Asp	His	Lys	Ala	Pro	Ala	Asp	Ser	Ser	Ser	Ser	Asn	Leu
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Asp	His	Tyr	Ser	Gly	Ser	Gln	Asp	Ser	Gln	Ser	Cys	Gly	Ser	Ala	Asp
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Ser	Gly	Ala	Asn	Gly	Cys	Ser	Gly	Arg	Gln	Ala	Ser	Ser	Pro	Gly	Thr
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Gln	Val	Asn	Pro	Leu	Gln	Met	Thr	Ala	Glu	Lys	Ile	Val	Asp	Gln	Ile
				165					170					175	
Val	Ser	Asp	Pro	Asp	Arg	Ala	Ser	Gln	Ala	Ile	Asn	Arg	Leu	Met	Arg
			180					185					190		
Thr	Gln	Lys	Glu	Ala	Ile	Ser	Val	Met	Glu	Lys	Val	Ile	Ser	Ser	Gln
		195					200						205		
Lys	Asp	Ala	Leu	Arg	Leu	Val	Ser	His	Leu	Ile	Asp	Tyr	Pro	Gly	Asp
		210				215					220				
Ala	Leu	Lys	Ile	Ile	Ser	Lys	Phe	Met	Asn	Ser	Pro	Phe	Asn	Ala	Leu
225					230					235					240
Thr	Val	Phe	Thr	Lys	Phe	Met	Ser	Ser	Pro	Thr	Asp	Gly	Val	Glu	Ile
				245					250					255	
Ile	Ser	Lys	Ile	Val	Asp	Ser	Pro	Ala	Asp	Val	Val	Glu	Phe	Met	Gln
			260					265					270		
Asn	Leu	Met	His	Ser	Pro	Glu	Asp	Ala	Ile	Asp	Ile	Met	Asn	Lys	Phe
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Met	Asn	Thr	Pro	Ala	Glu	Ala	Leu	Arg	Ile	Leu	Asn	Arg	Ile	Leu	Ser
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Gly	Gly	Gly	Ala	Asn	Ala	Gln	Gln	Thr	Ala	Asp	Arg	Lys	Pro	Leu	
305					310				315					320	
Leu	Asp	Lys	Glu	Pro	Ala	Val	Lys	Pro	Ala	Ala	Pro	Ala	Glu	Arg	Ala
				325					330					335	
Asp	Thr	Val	Ile	Gln	Ser	Met	Leu	Gly	Asn	Ser	Pro	Pro	Ile	Ser	Pro
			340					345					350		
His	Asp	Ala	Ala	Val	Asp	Leu	Gln	Tyr	His	Ser	Pro	Gly	Val	Gly	Glu
		355					360					365			
Gln	Pro	Ser	Thr	Ser	Ser	Ser	His	Pro	Leu	Pro	Tyr	Ile	Ala	Asn	Ser
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Pro	Asp	Phe	Asp	Leu	Lys	Thr	Phe	Met	Gln	Thr	Asn	Tyr	Asn	Asp	Glu
385					390					395					400
Pro	Ser	Leu	Asp	Ser	Asp	Phe	Ser	Ile	Asn	Ser	Ile	Glu	Ser	Val	Leu
				405					410					415	
Ser	Glu	Val	Ile	Arg	Ile	Glu	Tyr	Gln	Ala	Phe	Asn	Ser	Ile	Gln	Gln
			420						425					430	
Ala	Ala	Ser	Arg	Val	Lys	Glu	Glu	Met	Ser	Tyr	Gly	Thr	Gln	Ser	Thr
		435					440						445		
Tyr	Gly	Gly	Cys	Asn	Ser	Ala	Ala	Asn	Asn	Ser	Gln	Pro	His	Leu	Gln
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Leu	Tyr	Asp	Pro	Val	Asp	Glu	Asp	Leu	Ser	Ala	Leu	Met	Met	Gly	Asp
			500					505					510		
Asp	Arg	Ile	Lys	Pro	Asp	Asp	Thr	Arg	His	Asn	Pro	Lys	Leu	Leu	Gln
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 Lys Lys Ile Thr Ala Phe Arg Asp Met Cys Gln Glu Asp Gln Val Ala
 545 550 555 560
 Leu Leu Lys Gly Gly Cys Thr Glu Met Met Ile Met Arg Ser Val Met
 565 570 575
 Ile Tyr Asp Asp Arg Ala Ala Trp Lys Val Pro His Thr Lys Glu
 580 585 590
 Asn Met Gly Asn Ile Arg Thr Asp Leu Leu Lys Phe Ala Glu Gly Asn
 595 600 605
 Ile Tyr Glu Glu His Gln Lys Phe Ile Thr Thr Phe Asp Glu Lys Trp
 610 615 620
 Arg Met Asp Glu Asn Ile Leu Ile Met Cys Ala Ile Val Leu Phe
 625 630 635 640
 Thr Ser Ala Arg Ser Arg Val Ile His Lys Asp Val Ile Arg Leu Glu
 645 650 655
 Gln Asn Ser Tyr Tyr Tyr Leu Leu Arg Arg Tyr Leu Glu Ser Val Tyr
 660 665 670
 Ser Gly Cys Glu Ala Arg Asn Ala Phe Ile Lys Leu Ile Gln Lys Ile
 675 680 685
 Ser Asp Val Glu Arg Leu Asn Lys Phe Ile Ile Asn Val Tyr Leu Asn
 690 695 700
 Val Asn Pro Ser Gln Val Glu Pro Leu Leu Arg Glu Ile Phe Asp Leu
 705 710 715 720
 Lys Asn His

<210> 8

<211> 2832

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 8

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tcgactatcc aggcgacgca ctcaagatca tttcaaagtt tatgaactcg ccctttaacg     1020
cgctgacagt attcaccaaa ttcatgagct caccacgga cggcgttgaa attatctcaa     1080
agatagttga ttcgcccgcg gacgtggtgg agttcatgca gaacttgatg cactcgccag     1140
aggacgccat cgatataatg aacaagttca tgaatacccc agcggaggcg ctgcgcattc     1200
ttaaccgaat cctaagcggc ggaggagcga acgcagccca gcagacagca gaccgcaagc     1260
cattgctgga caaggagccg gcggtgaagc ctgcagcgcc agcggagcga gctgatactg     1320
tcattcaaaag catgctgggc aacagtcgcg caatttcgcc acatgatgct gccgtggatc     1380
tgcagtacca ctcgcccggg gtcgggggagc agcccagtag atcgagtagc cacccttgcc     1440

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cttacatagc caactcgccg gacttcgatc tgaagacctt catgcagacc aactacaacg      1500
acgagccagc tctggacagt gatttttagc ttaactcaat cgaatcgggtg ctatccgagg      1560
tgatccgcat tgagtaccag gccttcaata gcatacaaca agcggcatcg cgcgtaaagg      1620
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gccagccgca cctgcagcaa cccatctgcg ccccatccac ccagcagttg gatcgcgagc      1740
taaacgagggc ggagcaaagc aagctgcggg agctgcgact ggccagcgag gctctttatg      1800
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```

<210> 9

<211> 704

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 9

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1          5          10          15
Met Lys Val Asn Lys Val Glu Lys Met Glu Gln Glu Leu His Asp Pro
20          25          30
Glu Ser Glu Ser His Ile Met His Ala Asp Ala Leu Ala Ser Ala Tyr
35          40          45
Pro Ala Ala Ser Gln Pro His Ser Pro Ile Gly Leu Ala Leu Ser Pro
50          55          60
Asn Gly Gly Gly Leu Gly Leu Ser Asn Ser Ser Asn Gln Ser Ser Glu
65          70          75          80
Asn Phe Ala Leu Cys Asn Gly Asn Gly Asn Ala Gly Ser Ala Gly Gly
85          90          95
Gly Ser Ala Ser Ser Gly Ser Asn Asn Asn Asn Ser Met Phe Ser Pro
100         105         110
Asn Asn Asn Leu Ser Gly Ser Gly Ser Gly Thr Asn Ser Ser Gln Gln
115         120         125
Gln Leu Gln Gln Gln Gln Gln Gln Gln Ser Pro Thr Val Cys Ala Ile
130         135         140
Cys Gly Asp Arg Ala Thr Gly Lys His Tyr Gly Ala Ser Ser Cys Asp
145         150         155         160
Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Arg Lys Asn His Gln Tyr
165         170         175
Thr Cys Arg Phe Ala Arg Asn Cys Val Val Asp Lys Asp Lys Arg Asn
180         185         190
Gln Cys Arg Tyr Cys Arg Leu Arg Lys Cys Phe Lys Ala Gly Met Lys
195         200         205

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Lys Glu Ala Val Gln Asn Glu Arg Asp Arg Ile Ser Cys Arg Arg Thr
 210 215 220
 Ser Asn Asp Asp Pro Asp Pro Gly Asn Gly Leu Ser Val Ile Ser Leu
 225 230 235 240
 Val Lys Ala Glu Asn Glu Ser Arg Gln Ser Lys Ala Gly Ala Ala Met
 245 250 255
 Glu Pro Asn Ile Asn Glu Asp Leu Ser Asn Lys Gln Phe Ala Ser Ile
 260 265 270
 Asn Asp Val Cys Glu Ser Met Lys Gln Gln Leu Leu Thr Leu Val Glu
 275 280 285
 Trp Ala Lys Gln Ile Pro Ala Phe Asn Glu Leu Gln Leu Asp Asp Gln
 290 295 300
 Val Ala Leu Leu Arg Ala His Ala Gly Glu His Leu Leu Leu Gly Leu
 305 310 315 320
 Ser Arg Arg Ser Met His Leu Lys Asp Val Leu Leu Leu Ser Asn Asn
 325 330 335
 Cys Val Ile Thr Arg His Cys Pro Asp Pro Leu Val Ser Pro Asn Leu
 340 345 350
 Asp Ile Ser Arg Ile Gly Ala Arg Ile Ile Asp Glu Leu Val Thr Val
 355 360 365
 Met Lys Asp Val Gly Ile Asp Asp Thr Glu Phe Ala Cys Ile Lys Ala
 370 375 380
 Leu Val Phe Phe Asp Pro Asn Ala Lys Gly Leu Asn Glu Pro His Arg
 385 390 395 400
 Ile Lys Ser Leu Arg His Gln Ile Leu Asn Asn Leu Glu Asp Tyr Ile
 405 410 415
 Ser Asp Arg Gln Tyr Glu Ser Arg Gly Arg Phe Gly Glu Ile Leu Leu
 420 425 430
 Ile Leu Pro Val Leu Gln Ser Ile Thr Trp Gln Met Ile Glu Gln Ile
 435 440 445
 Gln Phe Ala Lys Ile Phe Gly Val Ala His Ile Asp Ser Leu Leu Gln
 450 455 460
 Glu Met Leu Leu Gly Gly Glu Leu Ala Asp Asn Pro Leu Pro Leu Ser
 465 470 475 480
 Pro Pro Asn Gln Ser Asn Asp Tyr Gln Ser Pro Thr His Thr Gly Asn
 485 490 495
 Met Glu Gly Gly Asn Gln Val Asn Ser Ser Leu Asp Ser Leu Ala Thr
 500 505 510
 Ser Gly Gly Pro Gly Ser His Ser Leu Asp Leu Glu Val Gln His Ile
 515 520 525
 Gln Ala Leu Ile Glu Ala Asn Ser Ala Asp Asp Ser Phe Arg Ala Tyr
 530 535 540
 Ala Ala Ser Thr Ala Ala Ala Ala Ala Val Ser Ser Ser Ser
 545 550 555 560
 Ser Ala Pro Ala Ser Val Ala Pro Ala Ser Ile Ser Pro Pro Leu Asn
 565 570 575
 Ser Pro Lys Ser Gln His Gln His Gln Gln His Ala Thr His Gln Gln
 580 585 590
 Gln Gln Glu Ser Ser Tyr Leu Asp Met Pro Val Lys His Tyr Asn Gly
 595 600 605
 Ser Arg Ser Gly Pro Leu Pro Thr Gln His Ser Pro Gln Arg Met His
 610 615 620
 Pro Tyr Gln Arg Ala Val Ala Ser Pro Val Glu Val Ser Ser Gly Gly
 625 630 635 640
 Gly Gly Leu Gly Leu Arg Asn Pro Ala Asp Ile Thr Leu Asn Glu Tyr
 645 650 655
 Asn Arg Ser Glu Gly Ser Ser Ala Glu Glu Leu Leu Arg Arg Thr Pro
 660 665 670
 Leu Lys Ile Arg Ala Pro Glu Met Leu Thr Ala Pro Ala Gly Tyr Gly
 675 680 685

Thr Glu Pro Cys Arg Met Thr Leu Lys Gln Glu Pro Glu Thr Gly Tyr
 690 695 700

<210> 10
 <211> 3248
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 10
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 caactgccct gcaaaagtca ctcatataat aaaaaacgcc cgagatgaat ttcacagcgg 180
 cggcaacaag tgcaataata gtaaaaaatc aaaagccaaa caacgaaatc tctcccaaaa 240
 aaacgaagaa gcgtgtcgcg gtgcacaaaa gaaaacaaaa atagaaaaat acacaacaaa 300
 ataatacggg gaaacgttaa ttataacgag ccacaaaatc gcataaagaa atcaacaagt 360
 gtgtgtctgc ctttttttcc atattcgctt tcattcatgc ggtcaactca acaataacaa 420
 ctcaaaatag caacaacaac aataacaata tcaacaagag cagcagcagt cgctgataaa 480
 agccctgcag ctaaaacaac aacaaaacaa caagatagt tagaaagaac atcgtctggc 540
 cattgagctt taattgccgg tcattacttc attactatgt gattggatct tcccgaccca 600
 cttgtaaaata aaaagtaaaa atactgggtta tgaagcatga tgaagcatcc gcaggatctg 660
 agtgtcacgg atgaccagca gttaatgaag gtgaacaagg tggagaagat ggagcaggag 720
 ttgcacgacc ccgaatcgga gagccacata atgcacgcgg atgccctggc ctctgcctat 780
 ccggtctgct cgcagcccca cagtccgcat ggcctcgccc tcagccccaa tggcggtggg 840
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 ggaaatgcgg gcagcgcagg aggcggaagt gccagcagtg gcagcaacaa caacaacagc 960
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 caggccctct cttgctgtac tccccaccaa gtgctatata gagatgaaat tgaaatgaag 2880


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aacttactta attgttatgc cttgaaccat tttgatactt tttattagtc ctaagtaggt 2940
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catatTTTgc tcaagaagtt tattatatac aattatacta tatatataca ccatttagca 3060
tgtactgagt ttgttggtta tttggttatc ttatacttgt gcgtggatca caaaacattc 3120
atataaggcc atgcaatata ttgtTTtagg ttaggggtgt gtctagatta tgctgaaagt 3180
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<210> 11

<211> 556

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 11

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Met Asp Glu Asp Cys Phe Pro Pro Leu Ser Gly Gly Trp Ser Ala Ser
1      5      10      15
Pro Pro Ala Pro Ser Gln Leu Gln Gln Leu His Thr Leu Gln Ser Gln
20     25     30
Ala Gln Met Ser His Pro Asn Ser Ser Asn Asn Ser Ser Asn Asn Ala
35     40     45
Gly Asn Ser His Asn Asn Ser Gly Gly Tyr Asn Tyr His Gly His Phe
50     55     60
Asn Ala Ile Asn Ala Ser Ala Asn Leu Ser Pro Ser Ser Ser Ala Ser
65     70     75     80
Ser Leu Tyr Glu Tyr Asn Gly Val Ser Ala Ala Asp Asn Phe Tyr Gly
85     90     95
Gln Gln Gln Gln Gln Gln Gln Ser Tyr Gln Gln His Asn Tyr Asn
100    105    110
Ser His Asn Gly Glu Arg Tyr Ser Leu Pro Thr Phe Pro Thr Ile Ser
115    120    125
Glu Leu Ala Ala Ala Thr Ala Ala Val Glu Ala Ala Ala Ala Thr
130    135    140
Val Ser Ser Pro Ser Val Gly Gly Pro Pro Pro Val Arg Arg Ala Ser
145    150    155    160
Leu Pro Val Gln Arg Thr Val Ser Pro Ala Gly Ser Thr Ala Gln Ser
165    170    175
Pro Lys Leu Ala Lys Ile Thr Leu Asn Gln Arg His Ser His Ala His
180    185    190
Ala His Ala Leu Gln Leu Asn Ser Ala Pro Asn Ser Ala Ala Ser Ser
195    200    205
Pro Ala Ser Ala Asp Leu Gln Ala Gly Arg Leu Leu Gln Ala Pro Ser
210    215    220
Gln Leu Cys Ala Val Cys Gly Asp Thr Ala Ala Cys Gln His Tyr Gly
225    230    235    240
Val Arg Thr Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val Gln
245    250    255
Lys Gly Ser Lys Tyr Val Cys Leu Ala Asp Lys Asn Cys Pro Val Asp
260    265    270
Lys Arg Arg Arg Asn Arg Cys Gln Phe Cys Arg Phe Gln Lys Cys Leu
275    280    285
Val Val Gly Met Val Lys Glu Val Val Arg Thr Asp Ser Leu Lys Gly
290    295    300
Arg Arg Gly Arg Leu Pro Ser Lys Pro Lys Ser Pro Gln Glu Ser Pro
305    310    315    320
Pro Ser Pro Pro Ile Ser Leu Ile Thr Ala Leu Val Arg Ser His Val
325    330    335

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Asp Thr Thr Pro Asp Pro Ser Cys Leu Asp Tyr Ser His Tyr Glu Glu
 340 345 350
 Gln Ser Met Ser Glu Ala Asp Lys Val Gln Gln Phe Tyr Gln Leu Leu
 355 360 365
 Thr Ser Ser Val Asp Val Ile Lys Gln Phe Ala Glu Lys Ile Pro Gly
 370 375 380
 Tyr Phe Asp Leu Leu Pro Glu Asp Gln Glu Leu Leu Phe Gln Ser Ala
 385 390 395 400
 Ser Leu Glu Leu Phe Val Leu Arg Leu Ala Tyr Arg Ala Arg Ile Asp
 405 410 415
 Asp Thr Lys Leu Ile Phe Cys Asn Gly Thr Val Leu His Arg Thr Gln
 420 425 430
 Cys Leu Arg Ser Phe Gly Glu Trp Leu Asn Asp Ile Met Glu Phe Ser
 435 440 445
 Arg Ser Leu His Asn Leu Glu Ile Asp Ile Ser Ala Phe Ala Cys Leu
 450 455 460
 Cys Ala Leu Thr Leu Ile Thr Glu Arg His Gly Leu Arg Glu Pro Lys
 465 470 475 480
 Lys Val Glu Gln Leu Gln Met Lys Ile Ile Gly Ser Leu Arg Asp His
 485 490 495
 Val Thr Tyr Asn Ala Glu Ala Gln Lys Lys Gln His Tyr Phe Ser Arg
 500 505 510
 Leu Leu Gly Lys Leu Pro Glu Leu Arg Ser Leu Ser Val Gln Gly Leu
 515 520 525
 Gln Arg Ile Phe Tyr Leu Lys Leu Glu Asp Leu Val Pro Ala Pro Ala
 530 535 540
 Leu Ile Glu Asn Met Phe Val Thr Thr Leu Pro Phe
 545 550 555

<210> 12

<211> 5181

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
 synthetic construct

<400> 12

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cgccgcccc	acgcccactg	accaggtgct	gacctcaag	atggacgagg	actgcttccc	180
gcctctgtcc	ggcggtgga	gtgccagtcc	gcccgcctcc	tcccagctcc	agcagctgca	240
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cgcgggcaac	agccacaaca	acagtggggg	ctacaactac	cacggccact	tcaatgccat	360
caatgccagc	gccaatctgt	cgcccagctc	ctcgccagct	tccctctacg	aatataatgg	420
tgtttccgca	gcggacaact	tctacggaca	acagcagcag	cagcaacagc	aaagctatca	480
gcaacataac	tacaactcgc	acaatggcga	gcgttactcg	ctgcccacgt	ttcccacgat	540
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gcactcccat	gcccattgcc	atgccctaca	gctcaactcg	gcaccaatt	cggcggaag	780
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gaattgcccc	gtggacaaga	ggcgccgcaa	ccgttgccag	ttctgccggg	tccagaagtg	1020
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gagactgccc	tcaaaaccga	aatcgcccca	ggagtgcgca	ccatcaccac	ccatctcggt	1140
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gctgaccagc	tccgtggacg	tgatcaagca	gttcgccgag	aagattcccc	gctacttcga	1320

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cagccgcagc	ctgcacaacc	tggagatcga	catctccgcc	ttcgctgcc	tctgtgccct	1560
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cgacgtacta	actctcccaa	ctgcgaactc	taccaattaa	gagaaattcc	cagaaaatgt	3780
gtcaggagttt	caagcgctcc	catctcactt	gaaccaccc	aatcaacaaa	tacaaatcct	3840
aggggaagttg	agagggttcag	caaccataga	gcaatatattc	ataagaaaa	gcaccttaaa	3900
ttaccgaaaa	acatagatta	acctgatctt	gtaacgtttg	ggagcgataa	taagccagga	3960
ttaaacagga	acagttaggt	gaccaaatac	gttcgaaacg	agatgataga	taggttcggg	4020
ttcgaaaccc	taaacgcgat	gccatttttag	ccgttacaac	attggatatac	aaccatgcac	4080
atgaatatga	atatgaatat	gaatattata	gagatatatac	tagctatagg	aacctacttt	4140
gtacctacac	gacatggaaa	catcaaacct	acatgcataat	ttacacacat	atattttgaa	4200
tagagcgacg	actttttacaa	gttgcgtaga	aagctatagc	tatagcttga	tatggccatc	4260
ccagagcgag	catatacata	tattttgggt	tattgttctt	ttgtaatttt	ataaatgcat	4320
acatatattat	tgtactacgt	gaatgtcaag	tgtggattca	tattttttgag	atacagctac	4380
aaaacgaaac	aaaagaaaat	aaaacaaaac	agaagagtaa	acgtgaaatt	tttcgatgaa	4440
acaatttttaa	atgagaactt	tttaatatgt	ctattaaagg	atatacatat	acacactaac	4500
atacatatat	attttactat	gtaacggata	gaattaaagc	agatgcagcg	cataaagctt	4560
tatacaacaa	attgaaaagc	aacagaagaa	attggcacaa	attaaattta	tatagcataa	4620
ttagacgtcc	ttcgcaagat	aatgttatcc	gtaataagag	cgtcaatcgg	tacatcgggc	4680
gctatttccc	actacacccc	caaccacaca	atagataacc	taagctatgt	atgtacatta	4740
gctatgtata	tccagcccac	ttatgcgcct	actactagaa	atgcagaaag	cagaaagaga	4800
ggtgaaacct	atagacgcta	tcacaaatgt	ctatctgata	gacatcggta	ctaccaatgc	4860
tatatgtcca	ggtgtgtaat	tactctttaa	ttgatcgttt	catttaccag	ttaagaacct	4920
aaatcatata	agtggttatga	tggagaact	ataacttgca	attcaattaa	ctctgcaata	4980

```

cgataacaag caaagcgaat catttcattt cgatttaatc ttttaattata tataacttaaa 5040
cgatgtaagc ccaaaacaaa cgttttttct atatctgtct tttgagcaaa ttagttatac 5100
gcaaaaccaa accgtattta cataaatgta tacaaaacaa atcgtatatt ttcattgggt 5160
tgaaataaat acataaaaaca a 5181

```

<210> 13
 <211> 278
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 13

Met	Ser	Asn	Phe	Ser	Ala	Cys	Ala	Val	Cys	Gly	Asp	Gln	Ser	Ser	Gly
1				5					10				15		
Lys	His	Tyr	Gly	Val	Ser	Cys	Cys	Asp	Gly	Cys	Ser	Cys	Phe	Phe	Lys
			20					25				30			
Arg	Ser	Val	Arg	Arg	Gly	Ser	Ser	Tyr	Ala	Cys	Ile	Ala	Leu	Val	Gly
			35				40					45			
Asn	Cys	Val	Val	Asp	Lys	Ala	Arg	Arg	Asn	Trp	Cys	Pro	Ser	Cys	Arg
	50				55				60						
Phe	Gln	Arg	Cys	Leu	Ala	Val	Gly	Met	Asn	Ala	Ala	Ala	Val	Gln	Glu
65				70			75							80	
Glu	Arg	Gly	Pro	Arg	Asn	Gln	Gln	Val	Ala	Leu	Tyr	Arg	Thr	Gly	Arg
			85				90						95		
Arg	Gln	Ala	Pro	Pro	Ser	Gln	Ala	Ala	Pro	Ser	Pro	Thr	Pro	His	Ser
			100				105						110		
Gln	Ala	Leu	His	Phe	Gln	Ile	Leu	Ala	Gln	Ile	Leu	Val	Thr	Cys	Leu
	115					120						125			
Arg	Gln	Ala	Lys	Ala	Asn	Glu	Gln	Phe	Ala	Leu	Leu	Asp	Arg	Cys	Gln
	130				135						140				
Gln	Asp	Ala	Ile	Phe	Gln	Val	Val	Trp	Ser	Glu	Ile	Phe	Val	Leu	Arg
145				150					155					160	
Ala	Ser	His	Trp	Ser	Leu	Asp	Ile	Ser	Ala	Met	Ile	Asp	Gly	Cys	Gly
			165				170						175		
Asp	Glu	Gln	Leu	Lys	Arg	Leu	Ile	Cys	Glu	Ala	His	Gln	Leu	Arg	Ala
			180				185					190			
Asp	Val	Leu	Glu	Leu	Asn	Phe	Met	Glu	Ser	Leu	Ile	Leu	Cys	Arg	Lys
	195				200						205				
Glu	Leu	Ala	Ile	Asn	Ala	Glu	Tyr	Ala	Val	Ile	Leu	Gly	Ser	His	Ser
	210			215						220					
Lys	Ala	Ala	Leu	Ile	Ser	Leu	Ala	Arg	Tyr	Thr	Leu	Gln	Gln	Ser	Asn
225				230					235					240	
Tyr	Leu	Arg	Phe	Gly	Gln	Leu	Leu	Leu	Gly	Leu	Arg	Gln	Leu	Cys	Leu
			245					250					255		
Arg	Arg	Phe	Asp	Cys	Ala	Leu	Ser	Cys	Met	Phe	Arg	Ser	Val	Val	Arg
			260				265						270		
Asp	Ile	Leu	Lys	Thr	Leu										
	275														

<210> 14
 <211> 837
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =

synthetic construct

```

<400> 14
atgtcgaact tcagtgcctg cgcagtgtgc ggcgatcaga gctccgggaa gcactacggc      60
gtgtcctgct gcgatgggtg ctccctgcttt ttcaagcgga gcgtgcggcg cgggagcagc      120
tacgcctgca tcgctctggt cgggaactgt gtgggtggaca aggcgcggcg gaactggtgt      180
ccctccctgcc gcttccagcg atgcctggcc gtgggaatga acgctgctgc gggtcaggag      240
gagcgcggtc cgcgcaacca gcaggtggct ctctaccgca ctggccggag acaagctccg      300
ccatctcagg cggcgccatc cccgacgccc cactcccagg cgctgcactt ccagatcctc      360
gccagatcc ttgtcacgtg cctgcgccag gcgaaggcca acgagcagtt cgctctgttg      420
gatcgctgcc aacaagacgc catctttcag gtgggtgtgga gcgagatctt cgtcctgcga      480
gcgtcccact ggtctctgga catcagcgcc atgatcgacg gctgcggcga tgagcagctc      540
aaacggctca tttgcgaggc ccaccagcta agggccgacg tcctggaact caactttatg      600
gagtcacctaa tcctgtgcag aaaagaattg gccatcaatg cggagtatgc cgttatcctg      660
ggaagccact ctaaagccgc cctgatctcc ttagcccgtc acaccctgca gcaatccaac      720
tacctgcggc tcggacaact gtccttgggt ctgaggcagc tgtgcctgag gcgcttcgac      780
tgcgcgcttt cttgtatggt tcgcagcgctg gtcagggaca tottaaaaac acttttag      837

```

<210> 15

<211> 281

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 15

```

Met Gly Met Arg Arg Glu Ala Val Gln Arg Gly Arg Val Pro Pro Thr
1      5      10      15
Gln Pro Gly Leu Ala Gly Met His Gly Gln Tyr Gln Ile Ala Asn Gly
20     25     30
Asp Pro Met Gly Ile Ala Gly Phe Asn Gly His Ser Tyr Leu Ser Ser
35     40     45
Tyr Ile Ser Leu Leu Leu Arg Ala Glu Pro Tyr Pro Thr Ser Arg Tyr
50     55     60
Gly Gln Cys Met Gln Pro Asn Asn Ile Met Gly Ile Asp Asn Ile Cys
65     70     75     80
Glu Leu Ala Ala Arg Leu Leu Phe Ser Ala Val Glu Trp Ala Lys Asn
85     90     95
Ile Pro Phe Phe Pro Glu Leu Gln Val Thr Asp Gln Val Ala Leu Leu
100    105    110
Arg Leu Val Trp Ser Glu Leu Phe Val Leu Asn Ala Ser Gln Cys Ser
115    120    125
Met Pro Leu His Val Ala Pro Leu Leu Ala Ala Ala Gly Leu His Ala
130    135    140
Ser Pro Met Ala Ala Asp Arg Val Val Ala Phe Met Asp His Ile Arg
145    150    155    160
Ile Phe Gln Glu Gln Val Glu Lys Leu Lys Ala Leu His Val Asp Ser
165    170    175
Ala Glu Tyr Ser Cys Leu Lys Ala Ile Val Leu Phe Thr Thr Asp Ala
180    185    190
Cys Gly Leu Ser Asp Val Thr His Ile Glu Ser Leu Gln Glu Lys Ser
195    200    205
Gln Cys Ala Leu Glu Glu Tyr Cys Arg Thr Gln Tyr Pro Asn Gln Pro
210    215    220
Thr Arg Phe Gly Lys Leu Leu Leu Arg Leu Pro Ser Leu Arg Thr Val
225    230    235    240
Ser Ser Gln Val Ile Glu Gln Leu Phe Phe Val Arg Leu Val Gly Lys
245    250    255

```

Thr Pro Ile Glu Thr Leu Ile Arg Asp Met Leu Leu Ser Gly Asn Ser
 260 265 270
 Phe Ser Trp Pro Tyr Leu Pro Ser Met
 275 280

<210> 16
 <211> 2866
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 16

ctaaattggt	gttttcaaaa	gaaatgaatt	tctttccact	cctttcagaa	ttcaagaata	60
aatattgaag	caatatggct	tcccttggtc	aaaccgatca	atcggtgcaa	atctttcttc	120
aagcgctcgg	tgcgacgtaa	tctaacttac	tcttgccgcg	gcagcagaaa	ctgtcccata	180
gatcaacacc	atcgcaatca	atgtcaatat	tgtcgattga	agaagtgcct	caaaatgggc	240
atgagacgcg	aagctgttca	acgtggacgc	gtaccaacca	ctcagcccgg	tctggccggc	300
atgcatgggc	agtaccagat	tgccaacggg	gatcccatgg	gcattgccgg	ctttaacggg	360
cactcgtacc	tcagttccta	catctcgctc	ctgctgcggg	cggaaaccgta	tccgacttcg	420
cgatatggcc	agtgcattga	acccaacaac	attatgggca	tcgacaacat	ctgcgaactg	480
gccgcccgcg	tgctcttctc	ggcggtcgag	tgggccaaga	acataccctt	cttcccggag	540
ctgcaggtga	ccgaccaggt	ggccctgctc	cggctcgtct	ggtcagagct	cttcgtccta	600
aacgccagcc	agtgtcccat	gccgctccat	gtggcgccac	tgctggccgc	cggcggactt	660
catgcctccc	cgatggccgc	cgatcgtgtg	gtggccttca	tggaccacat	ccgcatcttc	720
caggagcagg	tggagaagct	gaaggcgctg	catgtcgact	ccgaggagta	ctcctgcctc	780
aaggcgatcg	tgctcttcc	caccgatgcc	tgcggcctgt	ccgatgtgac	gcacattgaa	840
tccctgcaag	agaagtgcga	gtgcgccctc	gaggaatact	gccggaccga	gtatcccaac	900
cagcccacga	gattcggcaa	gctgcttctc	agactgccat	cgctgcgaac	gggtctccta	960
caagtcattg	agcaattggt	ttttgtgcgt	ctagtcggaa	aaacgccaat	tgaaacgctg	1020
atacgcgata	tgctgctgag	cggcaacagt	ttctcctggc	cctatctgcc	ttcgatgtga	1080
cacacgatgt	ggcgccaatt	gacaacaact	tgatcatcgg	ccgcagctgt	ggcggctgca	1140
acgctcaaca	tcaattccgg	cggaggcggc	atcggcacgc	gcggcggggg	cagtggcagt	1200
ggcggtggcg	gtagtggagg	cgggtggcga	gtcggtggat	gtggcagcca	caacgttgct	1260
gctgccagtc	atgaccagct	cgccaatggt	gctgtcatgc	agcaaacata	cggcagcggc	1320
ggcagcagca	gcagcagcat	cagcggttgc	cacaacggta	acaacggcag	cggcggcagc	1380
atltgcaatc	agcagatcaa	caactacggc	aacaacagca	acaacaatgt	cggcaatcat	1440
atgagtgcag	gcagtttttt	cgggtgggtcc	aacaacagca	tccacagtag	tggcaatagc	1500
aataccgatt	atatgaccac	gccagccacc	gcttatgcga	caccagcgac	agcagccaca	1560
tccacggtga	acaccacaac	gatgctgtct	aattactgcg	atgccgccac	catgatgatg	1620
gccgctgctg	cagtcaatgc	aaatcaatgc	ctgcagcaac	atcaccagcg	catggtgctc	1680
gcgggcagca	gcaacagcag	cagcaacaac	agcagcagca	acagcaacgg	cgcagcagca	1740
atgcccctct	catctctgtc	tggctcactg	tcatctgcct	catcgacccc	aacagcaaca	1800
gcaactgcga	ctgcaattgc	aacagcaaca	gcaactgcag	cagcaacagc	cgcgcagcaa	1860
caacagcaac	aatcgccgcc	aaatttaatc	gatatcagcg	aagttcctct	cattgtggat	1920
gtcaagtagt	gtgaattatt	atgcattctag	aaatggggct	ataaaccaac	cttgtagata	1980
ccccgccccg	ccccaccac	taccacaaaa	accataaaac	ccccaaaaaa	aaacaattga	2040
aaaatgtaaa	aaaaaaaaag	tggaggatga	gcgcgcgcta	gcttaattga	ctaattttcc	2100
atltgtagct	tttgtgttaa	ctttgtacat	aactcctcga	aaaattcaag	ttttctctta	2160
ggccaccccca	gctgtgagca	aaaccaatct	cagctgacat	atccaagaga	acttcaaaaag	2220
tgaagccccc	aaaaaaaagta	agaaggcgcc	aaaaaaacgt	ctttacatat	gaatgtgtat	2280
aataatttaaa	tggcactgag	ttctacttaa	tttttagacca	caaacacttg	aaaaaatcaa	2340
tgaaaaaata	agaattgtgg	aaagagaaaa	atccccctta	acactttcaa	aagacaaaac	2400
ataaagatag	ttaaaatatt	tatatatgta	atgtagcata	tacacgtata	tagtacatat	2460
atgaatatat	aaacgaaaact	ctactcccag	tggtttgcag	aaatatacca	aaaattttta	2520
gctatgttta	cttgatgtgt	ggcaattttt	atgtgtgctt	tagcaatttt	atttttactt	2580
taagtaaaat	ttaaaattta	taaacattcg	attctcgact	ggtttttctc	ggcggatgta	2640
tctcaaagat	gcttctgtat	gggaaggccg	aattgttgaa	atacgaatgc	aaaatttagc	2700

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gaatttttta ttttagtaacc attacgagta aaaacacaaa atgttcagtg caagtttcag 2760
ttcttaaacy attttttcgt aagcttaagc attatcttat ttatgtgtat agagtatgaa 2820
aagttttcta tattttgtaa taataaaaaat ttgcgtttat aatgaa 2866

```

<210> 17

<211> 452

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 17

```

Met Gln Ser Ser Glu Gly Ser Pro Asp Met Met Asp Gln Lys Tyr Asn
 1          5          10          15
Ser Val Arg Leu Ser Pro Ala Ala Ser Ser Arg Ile Leu Tyr His Val
 20          25          30
Pro Cys Lys Val Cys Arg Asp His Ser Ser Gly Lys His Tyr Gly Ile
 35          40          45
Tyr Ala Cys Asp Gly Cys Ala Gly Phe Phe Lys Arg Ser Ile Arg Arg
 50          55          60
Ser Arg Gln Tyr Val Cys Lys Ser Gln Lys Gln Gly Leu Cys Val Val
 65          70          75          80
Asp Lys Thr His Arg Asn Gln Cys Arg Ala Cys Arg Leu Arg Lys Cys
 85          90          95
Phe Glu Val Gly Met Asn Lys Asp Ala Val Gln His Glu Arg Gly Pro
100          105          110
Arg Asn Ser Thr Leu Arg Arg His Met Ala Met Tyr Lys Asp Ala Met
115          120          125
Met Gly Ala Gly Glu Met Pro Gln Ile Pro Ala Glu Ile Leu Met Asn
130          135          140
Thr Ala Ala Leu Thr Gly Phe Pro Gly Val Pro Met Pro Met Pro Gly
145          150          155          160
Leu Pro Gln Arg Ala Gly His His Pro Ala His Met Ala Ala Phe Gln
165          170          175
Pro Pro Pro Ser Ala Ala Ala Val Leu Asp Leu Ser Val Pro Arg Val
180          185          190
Pro His His Pro Val His Gln Gly His His Gly Phe Phe Ser Pro Thr
195          200          205
Ala Ala Tyr Met Asn Ala Leu Ala Thr Arg Ala Leu Pro Pro Thr Pro
210          215          220
Pro Leu Met Ala Ala Glu His Ile Lys Glu Thr Ala Ala Glu His Leu
225          230          235          240
Phe Lys Asn Val Asn Trp Ile Lys Ser Val Arg Ala Phe Thr Glu Leu
245          250          255
Pro Met Pro Asp Gln Leu Leu Leu Leu Glu Glu Ser Trp Lys Glu Phe
260          265          270
Phe Ile Leu Ala Met Ala Gln Tyr Leu Met Pro Met Asn Phe Ala Gln
275          280          285
Leu Leu Phe Val Tyr Glu Ser Glu Asn Ala Asn Arg Glu Ile Met Gly
290          295          300
Met Val Thr Arg Glu Val His Ala Phe Gln Glu Val Leu Asn Gln Leu
305          310          315          320
Cys His Leu Asn Ile Asp Ser Thr Glu Tyr Glu Cys Leu Arg Ala Ile
325          330          335
Ser Leu Phe Arg Lys Ser Pro Pro Ser Ala Ser Ser Thr Glu Asp Leu
340          345          350
Ala Asn Ser Ser Ile Leu Thr Gly Ser Gly Ser Pro Asn Ser Ser Ala
355          360          365

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```

Ser Ala Glu Ser Arg Gly Leu Leu Glu Ser Gly Lys Val Ala Ala Met
   370                               375                               380
His Asn Asp Ala Arg Ser Ala Leu His Asn Tyr Ile Gln Arg Thr His
385                               390                               395                               400
Pro Ser Gln Pro Met Arg Phe Gln Thr Leu Leu Gly Val Val Gln Leu
                               405                               410                               415
Met His Lys Val Ser Ser Phe Thr Ile Glu Glu Leu Phe Phe Arg Lys
                               420                               425                               430
Thr Ile Gly Asp Ile Thr Ile Val Arg Leu Ile Ser Asp Met Tyr Ser
                               435                               440                               445
Gln Arg Lys Ile
                               450

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<210> 18

<211> 1885

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 18

```

gagtcacacat cggagtaacc aaggatatat cgaatatatc acacaatccg caataccgcc      60
gtccacccaa accgttaaaa caaaaatcca aaacgactca aagatacacc agtgccaagt      120
gaaattcaat ttgtgcaagc gtttctacaa aaatcgccaa aattacgccc cacatcggtgta      180
tgcatcgctc ggaggggttca ccagacatga tggatcagaa atacaacagc gtgcgtcttt      240
cgccagcggc atcagagtcgc attctatacc atgtgccttg caaagtctgc agagatcaca      300
gctccggcaa gcattacggc atctacgcct gtgatggctg cgccggattc ttcaagagga      360
gcattcgag atcccggcag tatgtgtgca agtcgcagaa gcagggactc tgtgtggtgg      420
acaagacgea caggaacca ttagaggctt gccgactgag gaagtgcctt gaggtcggaa      480
tgaacaagga tgcagtgcag cagagcggg gaccgcgaa ctccactctg cgtcgccaca      540
tgcccatgta caaggatgcc atgatgggcg ccggcgagat gccacaaata cccgccgaaa      600
ttctgatgaa cacggctgcc ttgaccggct ttcttgagat accgatgcc atgcctggcc      660
tgccccagag ggctggtcat catcctgctc acatggctgc cttccagccg ccaccatcgg      720
ctgccgtgt cttggactta tccgtgccac gagtgcccca tcacccggtg caccaaggac      780
accacggttt cttctcgccc accgccgcct acatgaatgc cctggccact cgggccctgc      840
ccccactcc tccgtgatg gcagctgagc acatcaagga aaccgcggcg gaacacctat      900
tcaagaacgt caactggatc aagagcgtac gggccttcac cgaactgcc atgccggatc      960
agctgctcct gctggaggag tccctggaagg agttcttcat cctggccatg gcccagtacc     1020
taatgcccat gaatttcgcc cagctgctgt tcgtctacga gtccgagaat gccaacggg     1080
agatcatggg catggtgacc cgcgaggtgc acgccttcca ggaggtgctg aaccaactgt     1140
gccatctgaa cattgacagc accgagtagc agtgtctgag ggctatttcg ctcttccgta     1200
agtcaccacc gtoggcaagt tctaccgagg atttacgcaa cagctcaatc ctgacaggaa     1260
gcggcagccc gaactcctcg gcctctgctg aatccagggg tcttctggag tcgggaaaag     1320
tgggcgccat gcacaacgat gcccggagtg cgctgcacaa ctacatccag aggacccatc     1380
cctcgagccc catgcgattc cagacgctct tgggcgtggt gcagctgatg cacaaggctc     1440
caagcttcac catcgaggag ctgttcttcc gaaagaccat cggcgacatc accattgtgc     1500
gcctcatctc cgacatgtac agtcagcgca agatctgaaa agtatgtaga gcctagacta     1560
atgcgcgcac tcgaagtgcc ttccaagtgc tgggaactgt gataatctcg gaagaagcgc     1620
tttgacaat actcgatcag tgaaatcaac gatttctcat atccaggagt cgagccttaa     1680
aatacgtaca caacactcac cttaatacct tacctaaaca gaactcgaag taatcttagc     1740
taaagtctct cagaccatcc agatgtgttt caaattgcat tcgcaaaagt ttcaactttg     1800
cctgttaa at acgtcaatcg tagttttaa cactttagtt ttaagcgcat attattagct     1860
ttaggatttg gaaaaataat tatttc

```

<210> 19

<211> 691

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct.

<400> 19

```

Met Gly Thr Ala Gly Asp Arg Leu Leu Asp Ile Pro Cys Lys Val Cys
 1      5      10      15
Gly Asp Arg Ser Gly Lys His Tyr Gly Ile Tyr Ser Cys Asp Gly
 20      25      30
Cys Ser Gly Phe Phe Lys Arg Ser Ile His Arg Asn Arg Ile Tyr Thr
 35      40      45
Cys Lys Ala Thr Gly Asp Leu Lys Gly Arg Cys Pro Val Asp Lys Thr
 50      55      60
His Arg Asn Gln Cys Arg Ala Cys Arg Leu Ala Lys Cys Phe Gln Ser
 65      70      75      80
Ala Met Asn Lys Asp Ala Val Gln His Glu Arg Gly Pro Arg Lys Pro
 85      90      95
Lys Leu His Pro Gln Leu His His His His His His Ala Ala Ala Ala
100      105      110
Ala Ala Ala Ala His His Ala Ala Ala Ala His His His His His His
115      120      125
His His His Ala His Ala Ala Ala Ala His His Ala Ala Val Ala Ala
130      135      140
Ala Ala Ala Ser Gly Leu His His His His His Ala Met Pro Val Ser
145      150      155      160
Leu Val Thr Asn Val Ser Ala Ser Phe Asn Tyr Thr Gln His Ile Ser
165      170      175
Thr His Pro Pro Ala Pro Ala Ala Pro Pro Ser Gly Phe His Leu Thr
180      185      190
Ala Ser Gly Ala Gln Gln Gly Pro Ala Pro Pro Ala Gly His Leu His
195      200      205
His Gly Gly Ala Gly His Gln His Ala Thr Ala Phe His His Pro Gly
210      215      220
His Gly His Ala Leu Pro Ala Pro His Gly Gly Val Val Ser Asn Pro
225      230      235      240
Gly Gly Asn Ser Ser Ala Ile Ser Gly Ser Gly Pro Gly Ser Thr Leu
245      250      255
Pro Phe Pro Ser His Leu Leu His His Asn Leu Ile Ala Glu Ala Ala
260      265      270
Ser Lys Leu Pro Gly Ile Thr Ala Thr Ala Val Ala Ala Val Val Ser
275      280      285
Ser Thr Ser Thr Pro Tyr Ala Ser Ala Ala Gln Thr Ser Ser Pro Ser
290      295      300
Ser Asn Asn His Asn Tyr Ser Ser Pro Ser Pro Ser Asn Ser Ile Gln
305      310      315      320
Ser Ile Ser Ser Ile Gly Ser Arg Ser Gly Gly Gly Glu Glu Gly Leu
325      330      335
Ser Leu Gly Ser Glu Ser Pro Arg Val Asn Val Glu Thr Glu Thr Pro
340      345      350
Ser Pro Ser Asn Ser Pro Pro Leu Ser Ala Gly Ser Ile Ser Pro Ala
355      360      365
Pro Thr Leu Thr Thr Ser Ser Gly Ser Pro Gln His Arg Gln Met Ser
370      375      380
Arg His Ser Leu Ser Glu Ala Thr Thr Pro Pro Ser His Ala Ser Leu
385      390      395      400
Met Ile Cys Ala Ser Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
405      410      415
Asn Gly Glu His Lys Gln Ser Ser Tyr Thr Ser Gly Ser Pro Thr Pro
420      425      430
Thr Thr Pro Thr Pro Pro Pro Arg Ser Gly Val Gly Ser Thr Cys
435      440      445

```

Asn Thr Ala Ser Ser Ser Ser Gly Phe Leu Glu Leu Leu Leu Ser Pro
 450 455 460
 Asp Lys Cys Gln Glu Leu Ile Gln Tyr Gln Val Gln His Asn Thr Leu
 465 470 475 480
 Leu Phe Pro Gln Gln Leu Leu Asp Ser Arg Leu Leu Ser Trp Glu Met
 485 490 495
 Leu Gln Glu Thr Thr Ala Arg Leu Leu Phe Met Ala Val Arg Trp Val
 500 505 510
 Lys Cys Leu Met Pro Phe Gln Thr Leu Ser Lys Asn Asp Gln His Leu
 515 520 525
 Leu Leu Gln Glu Ser Trp Lys Glu Leu Phe Leu Leu Asn Leu Ala Gln
 530 535 540
 Trp Thr Ile Pro Leu Asp Leu Thr Pro Ile Leu Glu Ser Pro Leu Ile
 545 550 555 560
 Arg Glu Arg Val Leu Gln Asp Glu Ala Thr Gln Thr Glu Met Lys Thr
 565 570 575
 Ile Gln Glu Ile Leu Cys Arg Phe Arg Gln Ile Thr Pro Asp Gly Ser
 580 585 590
 Glu Val Gly Cys Met Lys Ala Ile Ala Leu Phe Ala Pro Glu Thr Ala
 595 600 605
 Gly Leu Cys Asp Val Gln Pro Val Glu Met Leu Gln Asp Gln Ala Gln
 610 615 620
 Cys Ile Leu Ser Asp His Val Arg Leu Arg Tyr Pro Arg Gln Ala Thr
 625 630 635 640
 Arg Phe Gly Arg Leu Leu Leu Leu Leu Pro Ser Leu Arg Thr Ile Arg
 645 650 655
 Ala Ala Thr Ile Glu Ala Leu Phe Phe Lys Glu Thr Ile Gly Asn Val
 660 665 670
 Pro Ile Ala Arg Leu Leu Arg Asp Met Tyr Thr Met Glu Pro Ala Gln
 675 680 685
 Val Asp Lys
 690

<210> 20

<211> 3043

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 20

gtcagcccag	gcgatccgca	tttgcgtccg	cagcaggttt	ccgatttcag	aactctgatt	60
ccagcggcag	cgaatcgcg	cggcatctga	acatttgaaa	ataatctaaa	attgcaagt	120
actttgtgca	ccggttacac	taaaattggt	aacaaatcgc	catatattct	gaatttaaat	180
ttaaagtgcg	cagtgcggaa	tataaatcag	agcaaactgg	ataggttagg	gttcaaatac	240
ttccatcaac	ggaaaatggg	cacagcgggc	gatcgccgtg	tggacattcc	ctgcaagggtg	300
tgtggcgatc	gcagctccgg	caagcactat	ggaatctaca	gctgcgatgg	ctgctccggt	360
tttttcaagc	ggagcattca	tcgcaatcgg	atttacacct	gtaaggccac	cggcgatctc	420
aagggtcgct	gtccggtgga	caagacccat	cggaatcagt	gtcgcgcctg	tcgcctggcc	480
aagtgtcttc	agtcggccat	gaacaaggat	gctgtgcagc	acgagcgcg	tcctaggaaa	540
cccaagttgc	acccgcaact	gcatcatcat	catcatcatg	ctgctgccgc	cgccgctgca	600
gcgcacatg	cagcagccgc	ccatcaccat	caccatcatc	accaccacgc	ccacgcagcg	660
gccgcccac	atgcggcagt	ggctgcagcg	gctgcctccg	ggctgcatca	ccaccaccac	720
gccatgcccg	tctcgctggt	gaccaatgtc	tcggcctcgt	tcaactatac	gcagcacatc	780
tccacgcac	cgcctgctcc	ggcggcgcca	cccagtggtc	ttcacctgac	ggccagtggc	840
gcccagcagg	gaccagctcc	accagctggc	cacctgcacc	atggtggagc	cggacatcag	900
cacgccacgg	ccttcaccac	tccgggacat	ggacacgcgc	tgccctgccc	acatggcgcg	960
gtcgtcagca	atcccggcgg	caactcgagc	gcaatctccg	gcagcggtcc	cggctccacg	1020
ctgcccttcc	cctcgcacct	gctgcaccac	aatctgatag	cggaggcggc	cagcaagctg	1080

```

ccgggcatca ctgccacagc cgttgcgggc gtggtgtcct ccactagcac gccctacgcc 1140
tcggcgggccc agacgtcgtc gcctagtagc aacaaccaca actactcttc gccctcgccc 1200
agcaactcca tccagtcctat ctcgagcatt ggatcgcgca gcggtggtgg cgaggagggc 1260
ctcagcctgg gcagcgagag tccgcgcgtc aatgtggaaa cggagacacc ttcgccatcg 1320
aactcgccgc cccttagtgc tggtagcatt tcgccagcgc ccacgttgac cacctcgtcg 1380
ggatcgccgc agcaccgcca gatgtcgcg cagagcctca gtgaggcaac cagcccgccc 1440
agccacgccc ctctcatgat ttgcgccagc aacaataaca ataacaacaa taataataac 1500
aataatggag agcacaagca gtcgagctac acatccggat caccgacacc cacaacgccc 1560
acgcccgcac cgcccggttc tgggtgtaggt tccacctgca acacggccag cagctccagc 1620
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cagcacaaca cgctgctctt cccgcaacag ctggttggaact cgcggtgct ctctggggag 1740
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atgccccttc agacgtctct caagaacgac cagcatttgc tgctccagga atcctggaag 1860
gagctcttcc tgctcaacct cgcccaatgg actataccgc tggatctaac gccatactg 1920
gaatcaccgc tcattccgca acgggtgctg caggacgagg ccacacaaac ggagatgaag 1980
acgatccagg agatcctctg ccgcttccgc cagatcacac ccgacggcag cgaggtgggg 2040
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gtggagatgt tgcaggatca ggcgcagtgc atcctctccg accatgtgcg actgcgctac 2160
cctcgccaag caaccgcgtt cggcaggctg ctgctcctgc tgccctcgct gcgcaccatc 2220
cggcgggcca ccattcgagg gctgttcttc aaggagacca tcggcaatgt gccattgct 2280
cgactgctgc gcgacatgta caccatggaa ccggcacagg tggacaagtg aaccggccac 2340
gcatgacagt cgaatgaaa tcaaaatcga ttccttagca cctaagcgcc acccatcggt 2400
cgtcgtcata tgcgaactta tttgtattcc aatgcgaccc gaatcctatt cagattcact 2460
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tggcgcactc ccacaccac acccgtaacc acaccttgat ttatcgccgg caatgcgtcg 2640
gagtctcctt actttcgctt cgttttctaa catttgatc cttattttat ttcattcttt 2700
tccacggatt tttcgtttg actgcctggg cggcactctt tatttatctt tcattcgacg 2760
ttttgtcgtc gcttttctaa aaattcccca tgttatttca acctggcaag gacctcgag 2820
tccattcccc gcgcccttac ttacaaatca cttcccatcc cacatccagc aattccgtgg 2880
tttgaattct ttcgtgcatt gactacgaaa taccctttaa tcagacaaat aaagaatatt 2940
agttgtaatt ctttttctg caatccagct ctaaacggg tttcttaatc gaaatcgata 3000
aatgtaaaaa ttatacatat cctttaccaa cattgtttgc cta 3043

```

<210> 21

<211> 532

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 21

```

Met Ala Thr Gly Arg Ser Leu Leu Phe Arg Val Pro Trp Tyr Val Cys
1           5           10           15
Leu Cys Val Cys Ala Glu Ser Ala Glu Pro Gly Val Tyr Trp Arg Leu
20           25           30
Arg Leu Arg Leu Gly Leu Pro Thr Leu Ala Gly Pro His Thr Asn Thr
35           40           45
Leu Thr Leu Thr Ala Arg Thr Ser Ser Cys Arg Ser Ile Lys Lys Glu
50           55           60
Arg Ile Lys Ala Ser Gln Gln Ala Asn Ala Pro Pro Glu Leu Pro Leu
65           70           75           80
Lys Val Ser Val Asp Val Asn Ile Ile Ile Ala Ala His Ser Gln Arg
85           90           95
Arg Arg Ile Gly Leu Val Arg Phe His Gln Arg Glu Ser Glu Asp Arg
100          105          110
Pro Leu Ala Val Ala Ser Pro Arg Leu Gln Ile Asn Met Glu Pro Thr
115          120          125

```

Ala Met Asn Pro Lys Lys Leu His Ser Pro Gln Arg His Cys Tyr Thr
 130 135 140
 Pro Pro Pro Ala Pro Met His Gly Gln Ala Pro Pro Pro Thr Ser Thr
 145 150 155 160
 Gly Val Ala Pro Pro Thr Gln Pro Pro Pro Pro His Pro Ala Ala Pro
 165 170 175
 Asn Val Pro Asn Gly Arg Leu Leu Ser Trp Asn His Ser Ala Ala Ala
 180 185 190
 Ala Ala Ala Ala Ala Ala Gln Ala Ala Ala Asn Ser Met Asn His
 195 200 205
 Ser Ser Ala Ala Glu Gly Ser Ser Met Thr Arg Ile Lys Gly Gln Asn
 210 215 220
 Leu Gly Leu Ile Cys Val Val Cys Gly Asp Thr Ser Ser Gly Lys His
 225 230 235 240
 Tyr Gly Ile Leu Ala Cys Asn Gly Cys Ser Gly Phe Phe Lys Arg Ser
 245 250 255
 Val Arg Arg Lys Leu Ile Tyr Arg Cys Gln Ala Gly Thr Gly Arg Cys
 260 265 270
 Val Val Asp Lys Ala His Arg Asn Gln Cys Gln Ala Cys Arg Leu Lys
 275 280 285
 Lys Cys Leu Gln Met Gly Met Asn Lys Asp Asp Asp Ser Ile Asp Val
 290 295 300
 Thr Asn Asp Asn Glu Glu Pro His Ala Val Ser Arg Ser Asp Ser Ser
 305 310 315 320
 Phe Ile Met Pro Gln Phe Met Ser Pro Asn Leu Tyr Thr His Gln His
 325 330 335
 Glu Thr Val Tyr Glu Thr Ser Ala Arg Leu Leu Phe Met Ala Val Lys
 340 345 350
 Trp Ala Lys Asn Leu Pro Ser Phe Ala Arg Leu Ser Phe Arg Asp Gln
 355 360 365
 Val Ile Leu Leu Glu Glu Ser Trp Ser Glu Leu Phe Leu Leu Asn Ala
 370 375 380
 Ile Gln Trp Cys Ile Pro Leu Asp Pro Thr Gly Cys Ala Leu Phe Ser
 385 390 395 400
 Val Ala Glu His Cys Asn Asn Leu Glu Asn Asn Ala Asn Gly Asp Thr
 405 410 415
 Cys Ile Thr Lys Glu Glu Leu Ala Ala Asp Val Arg Thr Leu His Glu
 420 425 430
 Ile Phe Cys Lys Tyr Lys Ala Val Leu Val Asp Pro Ala Glu Phe Ala
 435 440 445
 Cys Leu Lys Ala Ile Val Leu Phe Arg Pro Glu Thr Arg Gly Leu Lys
 450 455 460
 Asp Pro Ala Gln Ile Glu Asn Leu Gln Asp Gln Ala His His Thr Lys
 465 470 475 480
 Thr Gln Phe Thr Ala Gln Ile Ala Arg Phe Gly Arg Leu Leu Leu Met
 485 490 495
 Leu Pro Leu Leu Arg Met Ile Ser Ser His Lys Ile Glu Ser Ile Tyr
 500 505 510
 Phe Gln Arg Thr Ile Gly Asn Thr Pro Met Glu Lys Val Leu Cys Asp
 515 520 525
 Met Tyr Lys Asn
 530

<210> 22

<211> 1599

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
 synthetic construct

<400> 22

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atggcgaccg ggcgttctct gctctttcga gtgccttggt atgtgtgctt gtgtgtgtgc 60
gcagagagcg cagagccggg tgtttattgg agattgcgat tgcggcttgg cttaccacaca 120
ctcgcagggc cgcacaccaa cacactaaca ctaacagcga ggacaagctc ctgccgcagc 180
atcaagaagg aacgaatcaa agcaagccaa caagcaaatg cgccaccaga gttgccacta 240
aaagtctccg ttgacgttaa catcatcatc gcggcacact cgcagcgccg tcggatcgga 300
ttggttcggg ttcatcagcg ggaatcagag gaccgtccac ttgccgtcgc ctctccacga 360
ttgcaaatta atatggagcc tactgcgatg aacccgaaaa aactccacag tccgcagcgg 420
cattgtctaca ctccgcccgc ggcgcggatg cacggacagg cgcctccacc tacatcaacg 480
ggcgtggccc cgcccacaca gccaccgccc cctcatcccg cgccccaaaa cgtgcccatt 540
ggtcgattgc tgagctggaa tcacagtgcc gctgcagctg ctgcggcggc ggcagcccaa 600
gcggcagcca actccatgaa ccactcgtcg gcggcggagg gttcatcgat gaccgggatt 660
aagggtcaga acctgggctt catctgcgtg gtgtgcccgc acaccagctc gggaaagcac 720
tacggaatcc tagcctgcaa tggctgctcc ggattcttca aacgcagcgt gcggcggaaa 780
ctcattttatc gctgccaggc gggaaacggga cgctgtgttg tggacaaagc tcatcggaat 840
caatgccagg cctgcaggct caagaagtgc cttcaaattg gaatgaacaa ggacgacgac 900
tccatagatg taaccacga caacgaggag ccgcattgcg tcagcagatc ggattcgagt 960
ttcattatgc cgcagttcat gtcgcccatt ctgtacaccc atcaacacga aacagtttac 1020
gagacaagtg cccggtctgt cttcatggcc gtcaagtggg ccaagaacct gccagctttt 1080
gcaagacttt cctttcggga tcaggttaatt ttgctggagg agtcctggtc ggagctgttc 1140
ctgctgaacg caatccaatg gtgcattccc ctggatccca ccggtcgcgc cctcttctcg 1200
gtggcggagc actgcaataa tctagagaac aatgccaatg gcgacacttg cataacaaag 1260
gaggagctgg cggcggatgt gcgaacgctc cagcagatct tctgcaaata caaggcgggtg 1320
ctgggtggacc ccgctgaatt cgcgtgcctc aaggcgatag ttctcttccg gccggaaacg 1380
cgcggaacta aagatccggc gcagatagag aatcttcagg atcaggcgca ccacacaaag 1440
acgcagttca ccgccagat agccagattc ggacgactcc ttctcatgct gccgttgctg 1500
cgcatgatca gctccacaaa gattgagtc atctattttc agcgcaactat tgggaacacg 1560
cccattgaaa aggtgctctg tgacatgtat aagaactag 1599

```

<210> 23

<211> 484

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 23

```

Met Ser Asp Gly Val Ser Ile Leu His Ile Lys Gln Glu Val Asp Thr
1           5           10          15
Pro Ser Ala Ser Cys Phe Ser Pro Ser Ser Lys Ser Thr Ala Thr Gln
20          25          30
Ser Gly Thr Asn Gly Leu Lys Ser Ser Pro Ser Val Ser Pro Glu Arg
35          40          45
Gln Leu Cys Ser Ser Thr Thr Ser Leu Ser Cys Asp Leu His Asn Val
50          55          60
Ser Leu Ser Asn Asp Gly Asp Ser Leu Lys Gly Ser Gly Thr Ser Gly
65          70          75          80
Gly Asn Gly Gly Gly Gly Gly Gly Gly Thr Ser Gly Gly Asn Ala Thr
85          90          95
Asn Ala Ser Ala Gly Ala Gly Ser Gly Ser Val Arg Asp Glu Leu Arg
100         105         110
Arg Leu Cys Leu Val Cys Gly Asp Val Ala Ser Gly Phe His Tyr Gly
115         120         125
Val Ala Ser Cys Glu Ala Cys Lys Ala Phe Phe Lys Arg Thr Ile Gln
130         135         140
Gly Asn Ile Glu Tyr Thr Cys Pro Ala Asn Asn Glu Cys Glu Ile Asn
145         150         155         160

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Lys Arg Arg Arg Lys Ala Cys Gln Ala Cys Arg Phe Gln Lys Cys Leu
 165 170 175
 Leu Met Gly Met Leu Lys Glu Gly Val Arg Leu Asp Arg Val Arg Gly
 180 185 190
 Gly Arg Gln Lys Tyr Arg Arg Asn Pro Val Ser Asn Ser Tyr Gln Thr
 195 200 205
 Met Gln Leu Leu Tyr Gln Ser Asn Thr Thr Ser Leu Cys Asp Val Lys
 210 215 220
 Ile Leu Glu Val Leu Asn Ser Tyr Glu Pro Asp Ala Leu Ser Val Gln
 225 230 235 240
 Thr Pro Pro Pro Gln Val His Thr Thr Ser Ile Thr Asn Asp Glu Ala
 245 250 255
 Ser Ser Ser Ser Gly Ser Ile Lys Leu Glu Ser Ser Val Val Thr Pro
 260 265 270
 Asn Gly Thr Cys Ile Phe Gln Asn Asn Asn Asn Asn Asp Pro Asn Glu
 275 280 285
 Ile Leu Ser Val Leu Ser Asp Ile Tyr Asp Lys Glu Leu Val Ser Val
 290 295 300
 Ile Gly Trp Ala Lys Gln Ile Pro Gly Phe Ile Asp Leu Pro Leu Asn
 305 310 315 320
 Asp Gln Met Lys Leu Leu Gln Val Ser Trp Ala Glu Ile Leu Thr Leu
 325 330 335
 Gln Leu Thr Phe Arg Ser Leu Pro Phe Asn Gly Lys Leu Cys Phe Ala
 340 345 350
 Thr Asp Val Trp Met Asp Glu His Leu Ala Lys Glu Cys Gly Tyr Thr
 355 360 365
 Glu Phe Tyr Tyr His Cys Val Gln Ile Ala Gln Arg Met Glu Arg Ile
 370 375 380
 Ser Pro Arg Arg Glu Glu Tyr Tyr Leu Leu Lys Ala Leu Leu Leu Ala
 385 390 395 400
 Asn Cys Asp Ile Leu Leu Asp Asp Gln Ser Ser Leu Arg Ala Phe Arg
 405 410 415
 Asp Thr Ile Leu Asn Ser Leu Asn Asp Val Val Tyr Leu Leu Arg His
 420 425 430
 Ser Ser Ala Val Ser His Gln Gln Gln Leu Leu Leu Leu Leu Pro Ser
 435 440 445
 Leu Arg Gln Ala Asp Asp Ile Leu Arg Arg Phe Trp Arg Gly Ile Ala
 450 455 460
 Arg Asp Glu Val Ile Thr Met Lys Lys Leu Phe Leu Glu Met Leu Glu
 465 470 475 480
 Pro Leu Ala Arg

<210> 24

<211> 2529

<212> DNA

<213> Artificial Sequence

<220>

 <223> Description of Artificial Sequence; note =
 , synthetic construct

<400> 24

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ccctgggtcag gtctggttca ccaaaaaaga aaataaaatt acattttcaat ctttccaata      60
tgcaaatatc  tgcacgaaaa ccagcgagaa cagcatgctc acaataaaga gccccaaaac      120
aatgtgactc  gtatccgcgc agagtgcgtt ttcgtgcctt gcccgagtgc caaatccaaa      180
tcccaatcca  ggcgcacaaa atcgatgcag atgctgtctg cattctcata gaaagtgcaa      240
ctgaataacc  gatggtcgcc aaaagccacg atgtccagta ataatgacca gtgaataaac      300
aattatgact  cgagcatcga aaaatgctga ggaacgaata cataagcaat aacaagaagg      360
tgctcaactc  ggacccaaac aagtactaca tgctaacggt cgaggaggcc gatatgtatt      420
gacgttggtta cagtggagct gattacacaa aagatcctca gaacgatttt atccaaggca      480

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```

cgaacatgtc cgacggcgctc agcatcttgc acatcaaaaca ggaggtggac actccatcgg 540
cgctctgctt tagtcccagc tccaagtcaa cgccacgca gaggggcaca aacggcctga 600
aatcctcgcc ctcggtttcg ccggaaggc agctctgcag ctgcagacc tctctatcct 660
gcgatttgca caatgtatcc ttaagcaatg atggcgatag tctgaaagga agtggtagaa 720
gtggcgggcaa tggcgaggga ggaggtgggtg gtacgagtggt tggaaatgag accaatgcga 780
gtgcccggagc tggatcgagg tccgtcaggg acgagctccg ccgattgtgt ttggtttgtg 840
gcgatgtggc cagtggattc cactatgggtg tggcgagttg tgaggcttgc aaagcgttct 900
ttaaacgcac catccaaggc aacatcgagt acacgtgtcc ggcaacaac gagtgtgaga 960
ttaacaagcg gagacgcaag gcctgccaaag cgtgtcgctt ccagaaatgt ctactaatgg 1020
gcagtctcaa ggagggtgtg cgcttgatc gagttcgtgg aggacggcag aagtaccgaa 1080
ggaatcctgt atcaaaactct taccagacta tgcagctgct ataccaatcc aacaccacct 1140
cgctgtgcga tgtcaagata ctggaggtgc tcaattcata tgagccggat gccttgagcg 1200
tccaaacgcc gccgccgcaa gtccacacga ctagcataac taatgatgag gcctcatcct 1260
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aaaacaacaa caacaatgat cccaatgaga tactaagcgt ccttagtgat atttacgaca 1380
aggaattggt cagcgtcatt ggctgggcca agcagatacc tggctttata gatctgccac 1440
ttaacgacca gatgaagctt ctccaggtgt cgtgggcaga gatcctgacg ctccagctga 1500
ccttcgggtc cctaccgttc aatggcaagt tatgcttcgc cacggatgtc tggatggatg 1560
aacatttggc caaggagtgc ggttacacgg agttctacta ccactgcgtc cagatcgcac 1620
agcgcatgga aagaatatcg ccacgaaggg aggagtacta cttgctaaag gcgctcctgc 1680
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agcaacaatt gctgcttttg ctgccttcgc tgcggcaggc ggatgatata ctgcgaagat 1860
tttggcgtgg aattgcacgc gatgaagtca ttacatgaa gaaactgttc ctcgagatgc 1920
tcgagccgct ggccaggtga aaaggattat gcggcgccc aaactagttg atctagctga 1980
taagcaaagg tgcaaatata gtcttaggta tatatggatg tatactagag tagattaagc 2040
gtaggataag ccatgtatat aaatagtaaa atacttgtcg ggtaagatta gttcgcagaa 2100
aaaatctctt ttaatggact accaactaca gcaactggaa aaccctactt atcttctaga 2160
atcggggtgt gcttacactg gttaaaggcg catatagggtg ttatgtgtct aaagttgtga 2220
gtcacagatc ttcaataatt tgttcaattc tcaactgggtc tgatatatgt atatgccgca 2280
accttctgat gtaacgtatg aatttgtggg cactttttaa atagcatagt ggttctacaa 2340
tacaatggat tatactgttt ctaagtgtca tgaacccag tgattctgtg tctatgtggt 2400
acacatgcgg tcaaaaagaat agcaatgtcg tccgtgaata ataaaccgtt tgtaactgtt 2460
gtttccatac tccctaagtt ctgtattctt tggggatttt cttttcctaa acaaattcaa 2520
attagtttt 2529

```

<210> 25

<211> 601

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 25

```

Met Asp Gly Val Lys Val Glu Thr Phe Ile Lys Ser Glu Glu Asn Arg
1      5      10      15
Ala Met Pro Leu Ile Gly Gly Gly Ser Ala Ser Gly Gly Thr Pro Leu
20     25     30
Pro Gly Gly Gly Val Gly Met Gly Ala Gly Ala Ser Ala Thr Leu Ser
35     40     45
Val Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Arg His Tyr
50     55     60
Gly Ala Ile Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Ser Ile
65     70     75     80
Arg Lys Gln Leu Gly Tyr Gln Cys Arg Gly Ala Met Asn Cys Glu Val
85     90     95
Thr Lys His His Arg Asn Arg Cys Gln Phe Cys Arg Leu Gln Lys Cys
100    105    110

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Leu	Ala	Ser	Gly	Met	Arg	Ser	Asp	Ser	Val	Gln	His	Glu	Arg	Lys	Pro
	115						120					125			
Ile	Val	Asp	Arg	Lys	Glu	Gly	Ile	Ile	Ala	Ala	Ala	Gly	Ser	Ser	Ser
	130					135						140			
Thr	Ser	Gly	Gly	Gly	Asn	Gly	Ser	Ser	Thr	Tyr	Leu	Ser	Gly	Lys	Ser
	145				150					155					160
Gly	Tyr	Gln	Gln	Gly	Arg	Gly	Lys	Gly	His	Ser	Val	Lys	Ala	Glu	Ser
				165					170					175	
Ala	Ala	Thr	Pro	Pro	Val	His	Ser	Ala	Pro	Ala	Thr	Ala	Phe	Asn	Leu
			180					185					190		
Asn	Glu	Asn	Ile	Phe	Pro	Met	Gly	Leu	Asn	Phe	Ala	Glu	Leu	Thr	Gln
	195						200					205			
Thr	Leu	Met	Phe	Ala	Thr	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	His
	210					215					220				
Gln	Gln	Ser	Gly	Ser	Tyr	Ser	Pro	Asp	Ile	Pro	Lys	Ala	Asp	Pro	Glu
	225				230					235					240
Asp	Asp	Glu	Asp	Asp	Ser	Met	Asp	Asn	Ser	Ser	Thr	Leu	Cys	Leu	Gln
				245				250						255	
Leu	Leu	Ala	Asn	Ser	Ala	Ser	Asn	Asn	Ser	Gln	His	Leu	Asn	Phe	
		260					265					270			
Asn	Ala	Gly	Glu	Val	Pro	Thr	Ala	Leu	Pro	Thr	Thr	Ser	Thr	Met	Gly
		275					280					285			
Leu	Ile	Gln	Ser	Ser	Leu	Asp	Met	Arg	Val	Ile	His	Lys	Gly	Leu	Gln
	290					295					300				
Ile	Leu	Gln	Pro	Ile	Gln	Asn	Gln	Leu	Glu	Arg	Asn	Gly	Asn	Leu	Ser
	305				310					315					320
Val	Lys	Pro	Glu	Cys	Asp	Ser	Glu	Ala	Glu	Asp	Ser	Gly	Thr	Glu	Asp
				325					330					335	
Ala	Val	Asp	Ala	Glu	Leu	Glu	His	Met	Glu	Leu	Asp	Phe	Glu	Cys	Gly
			340					345					350		
Gly	Asn	Arg	Ser	Gly	Gly	Ser	Asp	Phe	Ala	Ile	Asn	Glu	Ala	Val	Phe
	355						360					365			
Glu	Gln	Asp	Leu	Leu	Thr	Asp	Val	Gln	Cys	Ala	Phe	His	Val	Gln	Pro
	370					375						380			
Pro	Thr	Leu	Val	His	Ser	Tyr	Leu	Asn	Ile	His	Tyr	Val	Cys	Glu	Thr
	385				390					395					400
Gly	Ser	Arg	Ile	Ile	Phe	Leu	Thr	Ile	His	Thr	Leu	Arg	Lys	Val	Pro
				405					410					415	
Val	Phe	Glu	Gln	Leu	Glu	Ala	His	Thr	Gln	Val	Lys	Leu	Leu	Arg	Gly
			420					425					430		
Val	Trp	Pro	Ala	Leu	Met	Ala	Ile	Ala	Leu	Ala	Gln	Cys	Gln	Gly	Gln
		435					440					445			
Leu	Ser	Val	Pro	Thr	Ile	Ile	Gly	Gln	Phe	Ile	Gln	Ser	Thr	Arg	Gln
	450					455					460				
Leu	Ala	Asp	Ile	Asp	Lys	Ile	Glu	Pro	Leu	Lys	Ile	Ser	Lys	Met	Ala
	465				470				475						480
Asn	Leu	Thr	Arg	Thr	Leu	His	Asp	Phe	Val	Gln	Glu	Leu	Gln	Ser	Leu
				485				490						495	
Asp	Val	Thr	Asp	Met	Glu	Phe	Gly	Leu	Leu	Arg	Leu	Ile	Leu	Leu	Phe
			500					505					510		
Asn	Pro	Thr	Leu	Leu	Gln	Gln	Arg	Lys	Glu	Arg	Ser	Leu	Arg	Gly	Tyr
		515					520					525			
Val	Arg	Arg	Val	Gln	Leu	Tyr	Ala	Leu	Ser	Ser	Leu	Arg	Arg	Gln	Gly
	530					535						540			
Gly	Ile	Gly	Gly	Gly	Glu	Glu	Arg	Phe	Asn	Val	Leu	Val	Ala	Arg	Leu
	545				550				555						560
Leu	Pro	Leu	Ser	Ser	Leu	Asp	Ala	Glu	Ala	Met	Glu	Glu	Leu	Phe	Phe
				565				570						575	
Ala	Asn	Leu	Val	Gly	Gln	Met	Gln	Met	Asp	Ala	Leu	Ile	Pro	Phe	Ile
			580					585					590		

Leu Met Thr Ser Asn Thr Ser Gly Leu
595 600

<210> 26
<211> 2288
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 26
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aaatatcgta actgaccgga agtaacataa ctttaaccaa gtgcctcgaa aaatagatgt 120
ttttaaaagc tcaagaatgg tgataacaga cgtccaataa gaattttcaa agagccaaat 180
gtttgggttt cagttattta tacagccgac gactattttt tagccgcctg ctgtggcgac 240
aatggacggc gtttaaggttg agacgttcat caaaagcgaa gaaaaccgag cgatgccttt 300
gatcggagga ggcagtgccct caggcggcac tcctctgccg ggaggcggcg tgggaatggg 360
agccggagca tccgcaacgt tgagcgtgga gctgtgtttg gtgtgcgggg accgcgcctc 420
cgggcccggc tacggagcca taagctgcga aggctgcaag ggattcttca agcgcctcat 480
ccggaagcag ctgggctacc agtgctgcgg ggctatgaac tgcgagggtca ccaagcacca 540
caggaatcgg tggcagttct gtcgactaca gaagtgcctg gccagcggca tgcgaagtga 600
ttctgtgcag cacgagagga aaccgattgt ggacaggaag gaggggatca tcgctgctgc 660
cggtagctca tccactttctg gcggcggtaa tggctcgtcc acctacctat ccggcaagtc 720
cggctatcag caggggcgtg gcaaggggca cagtgtaaag gccgaatccg cggccacgcc 780
tccagtgcac agcgcgccag caacggcctt caatttgaat gagaatatat tcccgatggg 840
tttgaatttc gcagaactaa cgcagacatt gatgttcgct acccaacagc agcagcaaca 900
acagcaacag catcaacaga gtggtagcta ttcgccagat attccgaagg cagatcccca 960
ggatgccag gacgactcaa tggacaacag cagcacgctg tgcttgcaat tgctcgccaa 1020
cagcgccagc aacaacaact cgcagcactt gaactttaat gctggggaag taccacccgc 1080
tctgcctacc acctcgacaa tggggcttat tcagagttcg ctggacatgc gggtcaccca 1140
caagggactg cagatcctgc agcccatcca aaaccaactg gagcgaatg gtaatctgag 1200
tgtgaagccc gagtgcgatt cagaggcggg ggacagtggt accgaggatg ccgtagacgc 1260
ggagctggag cacatggaac tagactttga gtgcggtggg aaccgaagcg gtggaagcga 1320
ttttgctatc aatgaggcgg tctttgaaca ggatcttctc accgatgtgc agtgcctt 1380
tcatgtgcaa ccgcccactt tgggtccactc gtattttaat attcattatg tgtgtgagac 1440
gggctcgcga atcatttttc tcaccatcca tacccttcga aaggttccag ttttcgaaca 1500
attggaagcc catacacagg tgaaactcct gagaggagtg tggccagcat taatggctat 1560
agctttggcg cagtgtcagg gtcagctttc ggtgccacc attatcgggc agtttattca 1620
aagcactcgc cagctagcgg atatcgataa gatcgaaccg ttgaagatct cgaagatggc 1680
aaatctcacc aggaccctgc acgactttgt ccaggagctc cagtcactgg atgttactga 1740
tatggagttt ggtttgctgc gtctgatctt gctcttcaat ccaacgctct tgcagcagcg 1800
caaggagcgg tcgttgcgag gctacgtccg cagagtccaa ctctacgctc tgtcaagttt 1860
gagaaggcag ggtggcatcg gcggcggcga ggagcgcttt aatgttctgg tggctcgcct 1920
tcttcgcctc agcagcctgg acgcagaggc catggaggag ctgttcttcg ccaacttggg 1980
ggggcagatg cagatggatg ctcttattcc gttcactact atgaccagca acaccagtgg 2040
actgtaggcg gaattgagaa gaacaggcgg caagcagatt cgctagactg cccaaaagca 2100
agactgaaga tggaccaagt gcgggcaata catgtagcaa ctaggcaaat ccattaatt 2160
atatatttta tatatacaat atatagttta ggatacaata ttctaacata aaaccatggg 2220
tttattgttg ttcacagata aatggaatc gatttcccaa taaaagcgaa tatgttttta 2280
aacagaat 2288

<210> 27
<211> 508
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 27

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Met Asp Asn Cys Asp Gln Asp Ala Ser Phe Arg Leu Ser His Ile Lys
 1          5          10          15
Glu Glu Val Lys Pro Asp Ile Ser Gln Leu Asn Asp Ser Asn Asn Ser
 20          25          30
Ser Phe Ser Pro Lys Ala Glu Ser Pro Val Pro Phe Met Gln Ala Met
 35          40          45
Ser Met Val His Val Leu Pro Gly Ser Asn Ser Ala Ser Ser Asn Asn
 50          55          60
Asn Ser Ala Gly Asp Ala Gln Met Ala Gln Ala Pro Asn Ser Ala Gly
 65          70          75          80
Gly Ser Ala Ala Ala Val Gln Gln Gln Tyr Pro Pro Asn His Pro
 85          90          95
Leu Ser Gly Ser Lys His Leu Cys Ser Ile Cys Gly Asp Arg Ala Ser
100          105          110
Gly Lys His Tyr Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly Phe Phe
115          120          125
Lys Arg Thr Val Arg Lys Asp Leu Thr Tyr Ala Cys Arg Glu Asn Arg
130          135          140
Asn Cys Ile Ile Asp Lys Arg Gln Arg Asn Arg Cys Gln Tyr Cys Arg
145          150          155          160
Tyr Gln Lys Cys Leu Thr Cys Gly Met Lys Arg Glu Ala Val Gln Glu
165          170          175
Glu Arg Gln Arg Gly Ala Arg Asn Ala Ala Gly Arg Leu Ser Ala Ser
180          185          190
Gly Gly Gly Ser Ser Gly Pro Gly Ser Val Gly Gly Ser Ser Ser Gln
195          200          205
Gly Gly Gly Gly Gly Gly Val Ser Gly Gly Met Gly Ser Gly Asn
210          215          220
Gly Ser Asp Asp Phe Met Thr Asn Ser Val Ser Arg Asp Phe Ser Ile
225          230          235          240
Glu Arg Ile Ile Glu Ala Glu Gln Arg Ala Glu Thr Gln Cys Gly Asp
245          250          255
Arg Ala Leu Thr Phe Leu Arg Val Gly Pro Tyr Ser Thr Val Gln Pro
260          265          270
Asp Tyr Lys Gly Ala Val Ser Ala Leu Cys Gln Val Val Asn Lys Gln
275          280          285
Leu Phe Gln Met Val Glu Tyr Ala Arg Met Met Pro His Phe Ala Gln
290          295          300
Val Pro Leu Asp Asp Gln Val Ile Leu Leu Lys Ala Ala Trp Ile Glu
305          310          315          320
Leu Leu Ile Ala Asn Val Ala Trp Cys Ser Ile Val Ser Leu Asp Asp
325          330          335
Gly Gly Ala Gly Gly Gly Gly Gly Gly Leu Gly His Asp Gly Ser Phe
340          345          350
Glu Arg Arg Ser Pro Gly Leu Gln Pro Gln Gln Leu Phe Leu Asn Gln
355          360          365
Ser Phe Ser Tyr His Arg Asn Ser Ala Ile Lys Ala Gly Val Ser Ala
370          375          380
Ile Phe Asp Arg Ile Leu Ser Glu Leu Ser Val Lys Met Lys Arg Leu
385          390          395          400
Asn Leu Asp Arg Arg Glu Leu Ser Cys Leu Lys Ala Ile Ile Leu Tyr
405          410          415
Asn Pro Asp Ile Arg Gly Ile Lys Ser Arg Ala Glu Ile Glu Met Cys
420          425          430
Arg Glu Lys Val Tyr Ala Cys Leu Asp Glu His Cys Arg Leu Glu His
435          440          445
Pro Gly Asp Asp Gly Arg Phe Ala Gln Leu Leu Leu Arg Leu Pro Ala
450          455          460

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Leu Arg Ser Ile Ser Leu Lys Cys Gln Asp His Leu Phe Leu Phe Arg
 465 470 475 480
 Ile Thr Ser Asp Arg Pro Leu Glu Glu Leu Phe Leu Glu Gln Leu Glu
 485 490 495
 Ala Pro Pro Pro Pro Gly Leu Ala Met Lys Leu Glu
 500 505

<210> 28

<211> 2488

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 28

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aaaaatgtcg acgcgaaaaa aggtattttat tcattagtca gaaagtcttg cattctttgt      60
ttgttggtaa aaagcgcaat tgtttgaggg cgagcgaata aagtgcgctg ctccatcggc      120
tcaagattat gtaaatgcag caacgacccc accaacaacg aaactgcaac ctgctccact      180
tggcccaacg gaccaatagc ggacggacgg acacgggtgg gttggcaaag tgaaacccca      240
acagagaggg gaaagcgagc caagacacac cacatacaca cgaagagaac gagcaagaag      300
aaaccggtag gcggaggagg cgctgcccc agttcctcca atatacccag caccacatca      360
caagcccagg atggacaact gcgaccagga cgccagcttt cggctgagcc acatcaagga      420
ggaggtcaag ccggacatct cgcagctgaa cgacagcaac aacagcagct tttcgcccaa      480
ggccgagagt cccgtgccct tcatgcaggg catgtccatg gtccacgtgc tgcccggctc      540
caactccgcc agctccaaca acaacagcgc tggagatgcc caaatggcgc aggcgcccaa      600
ttcggctgga ggctctgccg ccgctgcagt ccagcagcag tatccgccta accatccgct      660
gagcggcagc aagcacctct gctctatttg cggggatcgg gccagtggca agcactacgg      720
cgtgtacagc tgtgagggct gcaagggtct ctttaaagcg acagtgcgca aggatctcac      780
atacgtctgc agggagaacc gcaactgcat catagacaag cggcagagga accgctgcc      840
gtactgccgc taccagaagt gcctaacctg cggcatgaag cgcaagcgg tccaggagga      900
gcgtcaacgc ggcgccgca atgcggcggg taggctcagc gccagcggag gcggcagtag      960
cgggtccagg ttggtagggc gatccagctc tcaaggcggg ggaggaggag gcggcgtttc      1020
tggcggaatg ggcagcggca acggttctga tgacttcatg accaatagcg tgtccaggga      1080
tttctcgatc gagcgcacat tagaggccga gcagcgagcg gagaccaat gcggcgatcg      1140
tgcactgacg ttcctgcgcg ttggtcccta ttccacagtc cagccggact acaagggtgc      1200
cgtgtcggcc ctgtgccaat tggccaacaa acagctcttc cagatggctg aatacgcgcg      1260
catgatgcgc cactttgccc aggtgccgct ggacgaccag gtgattctgc tgaaagccgc      1320
ttggatcgag ctgctcattg cgaacgtggc ctgggtgcagc atcgtttcgc tggatgacgg      1380
cgggtgccgc ggcggggggc gtggactagg ccacgatggc tcctttgagc gacgatcacc      1440
gggccttcag ccccgagcagc tgttcctcaa ccagagcttc tcgtaccatc gcaacagtgc      1500
gatcaaagcc ggtgtgtcag ccattcttcga ccgcatattg tcggagctga gtgtaaagat      1560
gaagcggctg aatctcgacc gacgcgagct gtctctgctt aaggccatca tactgtacaa      1620
cccgacata cgcgggatca agagccgggc ggagatcgag atgtgccgcg agaagggtga      1680
cgcttgccct gacgagcact gccgcctgga acatccgggc gacgatggac gctttgcgca      1740
actgctgctg cgtctgccc ctttgcgatc gatcagcctg aagtgccagg atcacctgtt      1800
cctcttcgcg attaccagcg accggccgct ggaggagctc tttctcgagc agctggaggc      1860
gccgcgcgca cccggccttg cgatgaaact ggagtagggc cccgactcta aagtctcccc      1920
cgttctccat ccgaaaaatg tttcattgtg attgcgtttg tttgcatttc tcctctctat      1980
cccttatacc ctacaaaagc cccctaatat tacgcaaaat gtgtatgtaa ttgtttattt      2040
tttttttatt acctaataat attattatta ttgatataga aaatgttttc ctttaagatga      2100
agattagcct cctcgacgtt tatgtcccag taaacgaaaa acaaacaaaa tccaaaactt      2160
gaaaagaaca caaacacga acgagaaaat gcacacaagc aaagtataag taaaagttaa      2220
actaaagcta aacgagtaaa gatattaaaa taacgggttaa aattaatgca tagttatgat      2280
ctcagacagt atgtaaacad acaaattcag cataaatata tatgtcagca ggcgcatatc      2340
tgccgtgctg gcccggttct aaatcaattg taataacttt ttaacataaa tttacccaaa      2400
acgttatcaa ttagatgcga gatacaaaaa tcaccgacga aaaccaacaa aatatatcta      2460
tgtataaaaa atataaactg cataacaa      2488

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<210> 29
 <211> 906
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 29
 Met Gly Glu Glu Leu Pro Ile Leu Lys Gly Ile Leu Lys Gly Asn Val
 1 5 10 15
 Asn Tyr His Asn Ala Pro Val Arg Phe Gly Arg Val Pro Lys Arg Glu
 20 25 30
 Lys Ala Arg Ile Leu Ala Ala Met Gln Gln Ser Thr Gln Asn Arg Gly
 35 40 45
 Gln Gln Arg Ala Leu Ala Thr Glu Leu Asp Asp Gln Pro Arg Leu Leu
 50 55 60
 Ala Ala Val Leu Arg Ala His Leu Glu Thr Cys Glu Phe Thr Lys Glu
 65 70 75 80
 Lys Val Ser Ala Met Arg Gln Arg Ala Arg Asp Cys Pro Ser Tyr Ser
 85 90 95
 Met Pro Thr Leu Leu Ala Cys Pro Leu Asn Pro Ala Pro Glu Leu Gln
 100 105 110
 Ser Glu Gln Glu Phe Ser Gln Arg Phe Ala His Val Ile Arg Gly Val
 115 120 125
 Ile Asp Phe Ala Gly Met Ile Pro Gly Phe Gln Leu Leu Thr Gln Asp
 130 135 140
 Asp Lys Phe Thr Leu Leu Lys Ala Gly Leu Phe Asp Ala Leu Phe Val
 145 150 155 160
 Arg Leu Ile Cys Met Phe Asp Ser Ser Ile Asn Ser Ile Ile Cys Leu
 165 170 175
 Asn Gly Gln Val Met Arg Arg Asp Ala Ile Gln Asn Gly Ala Asn Ala
 180 185 190
 Arg Phe Leu Val Asp Ser Thr Phe Asn Phe Ala Glu Arg Met Asn Ser
 195 200 205
 Met Asn Leu Thr Asp Ala Glu Ile Gly Leu Phe Cys Ala Ile Val Leu
 210 215 220
 Ile Thr Pro Asp Arg Pro Gly Leu Arg Asn Leu Glu Leu Ile Glu Lys
 225 230 235 240
 Met Tyr Ser Arg Leu Lys Gly Cys Leu Gln Tyr Ile Val Ala Gln Asn
 245 250 255
 Arg Pro Asp Gln Pro Glu Phe Leu Ala Lys Leu Leu Glu Thr Met Pro
 260 265 270
 Asp Leu Arg Thr Leu Ser Thr Leu His Thr Glu Lys Leu Val Val Phe
 275 280 285
 Arg Thr Glu His Lys Glu Leu Leu Arg Gln Gln Met Trp Ser Met Glu
 290 295 300
 Asp Gly Asn Asn Ser Asp Gly Gln Gln Asn Lys Ser Pro Ser Gly Ser
 305 310 315 320
 Trp Ala Asp Ala Met Asp Val Glu Ala Ala Lys Ser Pro Leu Gly Ser
 325 330 335
 Val Ser Ser Thr Glu Ser Ala Asp Leu Asp Tyr Gly Ser Pro Ser Ser
 340 345 350
 Ser Gln Pro Gln Gly Val Ser Leu Pro Ser Pro Pro Gln Gln Gln Pro
 355 360 365
 Ser Ala Leu Ala Ser Ser Ala Pro Leu Leu Ala Ala Thr Leu Ser Gly
 370 375 380
 Gly Cys Pro Leu Arg Asn Arg Ala Asn Ser Gly Ser Ser Gly Asp Ser
 385 390 395 400

Gly	Ala	Ala	Glu	Met	Asp	Ile	Val	Gly	Ser	His	Ala	His	Leu	Thr	Gln		
				405					410						415		
Asn	Gly	Leu	Thr	Ile	Thr	Pro	Ile	Val	Arg	His	Gln	Gln	Gln	Gln	Gln		
			420					425					430				
Gln	Gln	Gln	Gln	Ile	Gly	Ile	Leu	Asn	Asn	Ala	His	Ser	Arg	Asn	Leu		
		435					440					445					
Asn	Gly	Gly	His	Ala	Met	Cys	Gln	Gln	Gln	Gln	Gln	His	Pro	Gln	Leu		
	450					455					460						
His	His	His	Leu	Thr	Ala	Gly	Ala	Ala	Arg	Tyr	Arg	Lys	Leu	Asp	Ser		
465				470					475					480			
Pro	Thr	Asp	Ser	Gly	Ile	Glu	Ser	Gly	Asn	Glu	Lys	Asn	Glu	Cys	Lys		
			485					490						495			
Ala	Val	Ser	Ser	Gly	Gly	Ser	Ser	Ser	Cys	Ser	Ser	Pro	Arg	Ser	Ser		
			500					505					510				
Val	Asp	Asp	Ala	Leu	Asp	Cys	Ser	Asp	Ala	Ala	Ala	Asn	His	Asn	Gln		
	515					520						525					
Val	Val	Gln	His	Pro	Gln	Leu	Ser	Val	Val	Ser	Val	Ser	Pro	Val	Arg		
	530					535					540						
Ser	Pro	Gln	Pro	Ser	Thr	Ser	Ser	His	Leu	Lys	Arg	Gln	Ile	Val	Glu		
545					550				555					560			
Asp	Met	Pro	Val	Leu	Lys	Arg	Val	Leu	Gln	Ala	Pro	Pro	Leu	Tyr	Asp		
			565					570						575			
Thr	Asn	Ser	Leu	Met	Asp	Glu	Ala	Tyr	Lys	Pro	His	Lys	Lys	Phe	Arg		
			580					585					590				
Ala	Leu	Arg	His	Arg	Glu	Phe	Glu	Thr	Ala	Glu	Ala	Asp	Ala	Ser	Ser		
	595					600						605					
Ser	Thr	Ser	Gly	Ser	Asn	Ser	Leu	Ser	Ala	Gly	Ser	Pro	Arg	Gln	Ser		
	610				615						620						
Pro	Val	Pro	Asn	Ser	Val	Ala	Thr	Pro	Pro	Pro	Ser	Ala	Ala	Ser	Ala		
625					630					635				640			
Ala	Ala	Gly	Asn	Pro	Ala	Gln	Ser	Gln	Leu	His	Met	His	Leu	Thr	Arg		
			645					650					655				
Ser	Ser	Pro	Lys	Ala	Ser	Met	Ala	Ser	Ser	His	Ser	Val	Leu	Ala	Lys		
		660						665				670					
Ser	Leu	Met	Ala	Glu	Pro	Arg	Met	Thr	Pro	Glu	Gln	Met	Lys	Arg	Ser		
	675						680					685					
Asp	Ile	Gln	Asn	Tyr	Leu	Lys	Arg	Glu	Asn	Ser	Ser	Thr	Ala	Ala	Ser		
	690				695					700							
Ser	Thr	Thr	Asn	Gly	Val	Gly	Asn	Arg	Ser	Pro	Ser	Ser	Ser	Ser	Thr		
705				710				715						720			
Pro	Pro	Pro	Ser	Ala	Val	Gln	Asn	Gln	Gln	Arg	Trp	Gly	Ser	Ser	Ser		
			725					730						735			
Val	Ile	Thr	Thr	Thr	Cys	Gln	Gln	Arg	Gln	Gln	Ser	Val	Ser	Pro	His		
			740					745					750				
Ser	Asn	Gly	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser		
	755						760					765					
Ser	Ser	Ser	Ser	Thr	Ser	Ser	Asn	Cys	Ser	Ser	Ser	Ser	Ala	Ser	Ser		
	770				775						780						
Cys	Gln	Tyr	Phe	Gln	Ser	Pro	His	Ser	Thr	Ser	Asn	Gly	Thr	Ser	Ala		
785					790				795					800			
Pro	Ala	Ser	Ser	Ser	Ser	Gly	Ser	Asn	Ser	Ala	Thr	Pro	Leu	Leu	Glu		
			805					810					815				
Leu	Gln	Val	Asp	Ile	Ala	Asp	Ser	Ala	Gln	Pro	Leu	Asn	Leu	Ser	Lys		
	820							825				830					
Lys	Ser	Pro	Thr	Pro	Pro	Pro	Ser	Lys	Leu	His	Ala	Leu	Val	Ala	Ala		
	835						840					845					
Ala	Asn	Ala	Val	Gln	Arg	Tyr	Pro	Thr	Leu	Ser	Ala	Asp	Val	Thr	Val		
	850				855						860						
Thr	Ala	Ser	Asn	Gly	Gly	Pro	Pro	Ser	Ala	Ala	Ala	Ser	Pro	Ala	Pro		
865					870				875					880			

Ser Ser Ser Pro Pro Ala Ser Val Gly Ser Pro Asn Pro Gly Leu Ser
 885 890 895
 Ala Ala Val His Lys Val Met Leu Glu Ala
 900 905

<210> 30
 <211> 3750
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 30
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 accatatagc acagcgtacc gcactctggg tatattcgta acgcgctttg gcttttacag 120
 ttagtcgctg tcgagacctt gtogagtttt gtcatgttag ccagcgatcc gcgggatccg 180
 aaataagcca agaatcacaa cgcgagtgcg gcagttgcca gcagtaacta caccaatatt 240
 tatattaatt aaaataaatt aaatgaaaca acatgctgat taatgccaat gaatgttaaa 300
 tgcaattggt aatgtgaaga aaagtcgacc aagtctcccc aaaacaacac ttattcaaca 360
 tccactacac actcgctttt ctggattacg cgcccaaaaa aaaacaaaaa ttaaaaatta 420
 aaccaaacca acaactaatt ttttgctaa atattccaaa aattcaatca atgtgaaaag 480
 caagcaacaa aagttcctct cacaacaaaa cagcagttaa ttaaaatatt taaccgagat 540
 aaagtgcaca gaagataaca agttttctca gcaaacatcc atatgtacct gagtaccaac 600
 caaaaagctg tgtgtgtgcc aaaaaccgaa gaggaattat ccaaaaatat ttaatgagca 660
 agctcaactg agtggttgat gtgcccccca agggaaaagt gaccaagtca agatattttg 720
 tcaaatcgaa cacagaaaac acaaaaatgg gcgaagaact cccgatattg aagggcatac 780
 ttaaaggcaa cgtcaactat cacaatgcgc ctgtgcgttt tggacgcgtg ccgaagcgcg 840
 aaaaggcgcg tatcctggcg gccatgcaac agagcaccga gaatcgcgcg cagcagcgag 900
 ccctcgccac cgagctggat gaccagccac gcctcctcgc cgccgtgctg cgcccccacc 960
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 gccctccta tcccatgccc acactcttgg cctgtccgct gaaccccgcc cctgaactgc 1080
 aatcgagcaa ggagttctcg cagcgtttcg ccacgtaat tcgcggcgtg atcgactttg 1140
 ccggcatgat tccgggcttc cagctgctca ccaggacga taagttcacg ctctgaagg 1200
 cgggactctt cgacgcctcg tttgtgcgcc tgatctgcat gtttgactcg tcgataaact 1260
 caatcatctg tctaaatggc caggtgatgc gacgggatgc gatccagaac ggagccaatg 1320
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 catagccga gataggtctg ttctgcgcca tcgttctgat tacgccgat cgccccggtt 1440
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 ccgatctgcg caccctgagc accctgcaca ccgagaaact ggtagttttc cgcaccgagc 1620
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 agcagaacaa gtgcgcctcg ggcagctggg cggatgccat ggacgtggag gcggccaaga 1740
 gtccgcttgg ctccgtatcg agcactgagt ccgccgacct ggactacggc agtccgagca 1800
 gttcgagcc acagggcggt tctctgccct cgccgcctca gcaacagccc tcggctctgg 1860
 ccagctcggc tctctgctg gcggccaccc tctccggagg atgtcccctg cgcaaccggg 1920
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 cacatctcac ccagaacggg ctgacaatca cgccgattgt gcgacaccag cagcagcaac 2040
 aacagcagca gcagatcgga atactcaata atgcgcattc ccgcaacttg aatgggggac 2100
 acgcgatgtg ccagcaacag cagcagcacc cacaactgca ccaccacttg acagccggag 2160
 ctgcccgtca cagaaaagcta gattcgccca cggattcggg cattgagtcg ggcaacgaga 2220
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 tgcacctgac ccgcagcagc cccaaggcct cgatggccag ctcgcactcg gtgctggcca 2760

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agacgtgtac aaagtttgaa agcaaaaacca acatgcagtc aatttaaaac taatatttaa 3660
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aacaacaaac ccaagcttga atggtattac 3750

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<210> 31

<211> 392

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 31

```

Met His Pro Ser His Leu Gln Gln Gln Gln Gln His Leu Leu Gln
1      5      10      15
Gln Gln Gln Gln Gln Gln His Gln Pro Gln Leu Gln Gln His His Gln
20     25     30
Leu Gln Gln Gln Pro His Val Ser Gly Val Arg Val Lys Thr Pro Ser
35     40     45
Thr Pro Gln Thr Pro Gln Met Cys Ser Ile Ala Ser Ser Pro Ser Glu
50     55     60
Leu Gly Gly Cys Asn Ser Ala Asn Asn Asn Asn Asn Asn Asn Asn
65     70     75     80
Ser Ser Ser Gly Asn Ala Ser Gly Gly Ser Gly Val Ser Val Gly Val
85     90     95
Val Val Val Gly Gly His Gln Gln Leu Val Gly Gly Ser Met Val Gly
100    105    110
Met Ala Gly Met Gly Thr Asp Ala His Gln Val Gly Met Cys His Asp
115    120    125
Gly Leu Ala Gly Thr Ala Asn Glu Leu Thr Val Tyr Asp Val Ile Met
130    135    140
Cys Val Ser Gln Ala His Arg Leu Asn Cys Ser Tyr Thr Glu Glu Leu
145    150    155    160
Thr Arg Glu Leu Met Arg Arg Pro Val Thr Val Pro Gln Asn Gly Ile
165    170    175
Ala Ser Thr Val Ala Glu Ser Leu Glu Phe Gln Lys Ile Trp Leu Trp
180    185    190
Gln Gln Phe Ser Ala Arg Val Thr Pro Gly Val Gln Arg Ile Val Glu
195    200    205
Phe Ala Lys Arg Val Pro Gly Phe Cys Asp Phe Thr Gln Asp Asp Gln
210    215    220
Leu Ile Leu Ile Lys Leu Gly Phe Phe Glu Val Trp Leu Thr His Val
225    230    235    240
Ala Arg Leu Ile Asn Glu Ala Thr Leu Thr Leu Asp Asp Gly Ala Tyr
245    250    255

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Leu Thr Arg Gln Gln Leu Glu Ile Leu Tyr Asp Ser Asp Phe Val Asn
 260 265 270
 Ala Leu Leu Asn Phe Ala Asn Thr Leu Asn Ala Tyr Gly Leu Ser Asp
 275 280 285
 Thr Glu Ile Gly Leu Phe Ser Ala Met Val Leu Leu Ala Ser Asp Arg
 290 295 300
 Ala Gly Leu Ser Glu Pro Lys Val Ile Gly Arg Ala Arg Glu Leu Val
 305 310 315 320
 Ala Glu Ala Leu Arg Val Gln Ile Leu Arg Ser Arg Ala Gly Ser Pro
 325 330 335
 Gln Ala Leu Gln Leu Met Pro Ala Leu Glu Ala Lys Ile Pro Glu Leu
 340 345 350
 Arg Ser Leu Gly Ala Lys His Phe Ser His Leu Asp Trp Leu Arg Met
 355 360 365
 Asn Trp Thr Lys Leu Arg Leu Pro Pro Leu Phe Ala Glu Ile Phe Asp
 370 375 380
 Ile Pro Lys Ala Asp Asp Glu Leu
 385 390

<210> 32

<211> 3341

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
 synthetic construct

<400> 32

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aatattatag	tattgggaat	attagggttac	ttgatatcaa	aaattaatgt	ctattttata	180
cacttattct	tagacttaat	gttaacttat	cgtacttatt	atgattgggt	tttcaagatt	240
accagaactt	gatagattgg	tctagctttt	gaaatcggat	agcattttct	ttaaaggact	300
ttgccatatg	ctaaagccta	acttcttttt	tcaattcagc	cacagctgac	aaaagcgaag	360
aaaatttgaa	agaccgtgaa	tccttttgaa	acgccctctc	cggattcctc	attaagtgca	420
aaagatataa	catcgagag	atttcccata	aaaatgctga	tcaggcgccc	tcgcagggtg	480
ccaacgctga	tttccgccag	caggacgatg	atgaagatga	tggatgcccc	tctcacccgat	540
tcgatccgag	caacatggat	gtataccaaa	tagagctgga	ggaacaggca	caaatccgct	600
ccaaactgct	ggtcgaaaacc	tgtgtgaagc	actcgtcttc	ggagcagcag	cagctccaag	660
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atagcttgga	atccgagcag	gaagaggaga	agcaaacaca	gcagcatcag	cagcagaagc	960
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gcccacagca	gcagcagcaa	cggcagcaca	cccaccagca	acaacagcaa	cagcagcagc	1140
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cacagctgca	acagcagcag	cagcaccagc	agcagttgca	acacccgcag	cagcagcaat	1560
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aatatcgctg	tttgcgggac	ggcaagtgcc	tggtcatcag	actgaaccgc	aatcgctgcc	1800
agtactgccg	cttcaagaaa	tgcttttccg	ctggcatgag	ccgcgattcc	gtacgttatg	1860
gtcgcggtcc	caagcgttcc	cgtgagctga	acggagcggc	cgccctcctc	gccgccgctg	1920


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gagctcctgc ctccctcaat gtggatgact ctaccagcag cacactgcac ccgagtcacc 1980
tacagcagca gcagcaacag catctactac agcagcaaca gcagcagcaa catcagccac 2040
agctgcagca acaccaccaa ctgcaacagc agccgcgatgt aagcggcgta cgtgtgaaga 2100
ccccgagtac tccacaaacg ccacaaatgt gttcgatcgc ctctcgcca tcggagctgg 2160
gcgggttgcaa tagtgccaat aacaataaca ataataacaa caacagtagc agcggtaatg 2220
ccagcgggtg cagcggcggtg agcgtcggcg ttgttgttgt gggcggacac cagcaactgg 2280
tgaggaggcag catggtggga atggcgggca tgggcacgga tgcccaccag gtgggcatgt 2340
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aagccaagat acccgagctg agatccttgg gggccaagca cttctcacac ctgactggc 3060
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gatcgaaatg ggagggccgc agatcagata cagctctact cagcattacc ggagagatag 3300
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<210> 33

<211> 878

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 33

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Met Lys Arg Arg Trp Ser Asn Asn Gly Gly Phe Met Arg Leu Pro Glu
1           5           10          15
Glu Ser Ser Ser Glu Val Thr Ser Ser Ser Asn Gly Leu Val Leu Pro
20          25          30
Ser Gly Val Asn Met Ser Pro Ser Ser Leu Asp Ser His Asp Tyr Cys
35          40          45
Asp Gln Asp Leu Trp Leu Cys Gly Asn Glu Ser Gly Ser Phe Gly Gly
50          55          60
Ser Asn Gly His Gly Leu Ser Gln Gln Gln Gln Ser Val Ile Thr Leu
65          70          75          80
Ala Met His Gly Cys Ser Ser Thr Leu Pro Ala Gln Thr Thr Ile Ile
85          90          95
Pro Ile Asn Gly Asn Ala Asn Gly Asn Gly Gly Ser Thr Asn Gly Gln
100         105         110
Tyr Val Pro Gly Ala Thr Asn Leu Gly Ala Leu Ala Asn Gly Met Leu
115         120         125
Asn Gly Gly Phe Asn Gly Met Gln Gln Gln Ile Gln Asn Gly His Gly
130         135         140
Leu Ile Asn Ser Thr Thr Pro Ser Thr Pro Thr Pro Leu His Leu
145         150         155         160
Gln Gln Asn Leu Gly Gly Ala Gly Gly Gly Gly Ile Gly Gly Met Gly
165         170         175
Ile Leu His His Ala Asn Gly Thr Pro Asn Gly Leu Ile Gly Val Val
180         185         190
Gly Gly Gly Gly Gly Val Gly Leu Gly Val Gly Gly Gly Val Gly
195         200         205

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Gly Leu Gly Met Gln His Thr Pro Arg Ser Asp Ser Val Asn Ser Ile
 210 215 220
 Ser Ser Gly Arg Asp Asp Leu Ser Pro Ser Ser Ser Leu Asn Gly Tyr
 225 230 235 240
 Ser Ala Asn Glu Ser Cys Asp Ala Lys Lys Ser Lys Lys Gly Pro Ala
 245 250 255
 Pro Arg Val Gln Glu Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser
 260 265 270
 Gly Tyr His Tyr Asn Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe
 275 280 285
 Arg Arg Ser Val Thr Lys Ser Ala Val Tyr Cys Cys Lys Phe Gly Arg
 290 295 300
 Ala Cys Glu Met Asp Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg
 305 310 315 320
 Leu Lys Lys Cys Leu Ala Val Gly Met Arg Pro Glu Cys Val Val Pro
 325 330 335
 Glu Asn Gln Cys Ala Met Lys Arg Arg Glu Lys Lys Ala Gln Lys Glu
 340 345 350
 Lys Asp Lys Met Thr Thr Ser Pro Ser Ser Gln His Gly Gly Asn Gly
 355 360 365
 Ser Leu Ala Ser Gly Gly Gly Gln Asp Phe Val Lys Lys Glu Ile Leu
 370 375 380
 Asp Leu Met Thr Cys Glu Pro Pro Gln His Ala Thr Ile Pro Leu Leu
 385 390 395 400
 Pro Asp Glu Ile Leu Ala Lys Cys Gln Ala Arg Asn Ile Pro Ser Leu
 405 410 415
 Thr Tyr Asn Gln Leu Ala Val Ile Tyr Lys Leu Ile Trp Tyr Gln Asp
 420 425 430
 Gly Tyr Glu Gln Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln
 435 440 445
 Pro Asp Glu Asn Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr
 450 455 460
 Glu Ile Thr Ile Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly
 465 470 475 480
 Leu Pro Ala Phe Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu
 485 490 495
 Lys Ala Cys Ser Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr
 500 505 510
 Asp His Ser Ser Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr
 515 520 525
 Arg Asp Ser Tyr Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu
 530 535 540
 Leu His Phe Cys Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu
 545 550 555 560
 Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu
 565 570 575
 Glu Lys Ala Gln Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr
 580 585 590
 Leu Arg Ile Tyr Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu
 595 600 605
 Val Phe Tyr Ala Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu
 610 615 620
 Gly Asn Gln Asn Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg
 625 630 635 640
 Lys Leu Pro Lys Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro
 645 650 655
 Pro Ser Val Gln Ser His Leu Gln Ile Thr Gln Glu Glu Asn Glu Arg
 660 665 670
 Leu Glu Arg Ala Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr
 675 680 685

Ala Gly Ile Asp Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala
 690 695 700
 Ala Gln His Gln Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu
 705 710 715 720
 Thr Gln Asn Asp Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln
 725 730 735
 Leu Pro Pro Gln Leu Gln Gly, Gln Leu Gln Pro Gln Leu Gln Pro Gln
 740 745 750
 Leu Gln Thr Gln Leu Gln Pro Gln Ile Gln Pro Gln Pro Gln Leu Leu
 755 760 765
 Pro Val Ser Ala Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu
 770 775 780
 Ser Ala Val Ser Thr Ser Ser Glu Tyr Met Gly Gly Ser Ala Ala Ile
 785 790 795 800
 Gly Pro Ile Thr Pro Ala Thr Thr Ser Ser Ile Thr Ala Ala Val Thr
 805 810 815
 Ala Ser Ser Thr Thr Ser Ala Val Pro Met Gly Asn Gly Val Gly Val
 820 825 830
 Gly Val Gly Val Gly Gly Asn Val Ser Met Tyr Ala Asn Ala Gln Thr
 835 840 845
 Ala Met Ala Leu Met Gly Val Ala Leu His Ser His Gln Glu Gln Leu
 850 855 860
 Ile Gly Gly Val Ala Val Lys Ser Glu His Ser Thr Thr Ala
 865 870 875

<210> 34

<211> 5586

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
 synthetic construct

<400> 34

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gtacggtttc	ccaaagcacc	ttacatttca	aaaccgaaaa	cccccaaat	gttgtaacca	180
aataatgttt	aaatcacata	tacacctaca	tatatattatg	aaaaattggt	agacaaatcc	240
caaataatc	cagttccccc	aacaaccgca	acaaacacaa	gtgcaattca	tcggcaaaaa	300
ttaatataaa	gtgcaaatgc	attgtagctg	aaactcaaac	aatagtaaaa	atacatatcat	360
aagtgggtgaa	gaagcaaaag	gaaatagttc	ttaaaataac	gcaaatacgag	agcatatatatt	420
catatttgta	cagatattat	atggcggctg	catagtgcga	actgcggctg	aggggaatata	480
gcgggtatcga	aatgtaaata	ggaaacaacg	aagccagaac	tcgaaatcaa	acatcagcaa	540
cgtgacacac	agacataaga	cgcccgctcta	gtcgtggctc	gtggaacgct	agctccgctt	600
tgccaggagc	cggagacttt	ttccgcatcc	acaatattac	atatgtacat	atatcgaaga	660
tagtgcgcg	gtgagtgagg	gatttgtgcc	gtggatcccg	atcccccttac	atatatataa	720
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<210> 35

<211> 808

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 35

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Val Ala Asn Thr Thr Thr Thr Leu Gly Ser Ser Ala Gly Gly Ala Thr
      35      40      45
Gly Ser Arg His Asn Val Ser Val Thr Asn Ile Lys Cys Glu Leu Asp
      50      55      60
Glu Leu Pro Ser Pro Asn Gly Asn Met Val Pro Val Ile Ala Asn Tyr
      65      70      75      80
Val His Gly Ser Leu Arg Ile Pro Leu Ser Gly His Ser Asn His Arg
      85      90      95
Glu Ser Asp Ser Glu Glu Glu Leu Ala Ser Ile Glu Asn Leu Lys Val
      100     105     110
Arg Arg Arg Thr Ala Ala Asp Lys Asn Gly Pro Arg Pro Met Ser Trp
      115     120     125
Glu Gly Glu Leu Ser Asp Thr Glu Val Asn Gly Gly Glu Glu Leu Met
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Glu Met Glu Pro Thr Ile Lys Ser Glu Val Val Pro Ala Val Ala Pro
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Pro Gln Pro Val Cys Ala Leu Gln Pro Ile Lys Thr Glu Leu Glu Asn
      165     170     175
Ile Ala Gly Glu Met Gln Ile Gln Glu Lys Cys Tyr Pro Gln Ser Asn
      180     185     190
Thr Gln His His Ala Ala Thr Lys Leu Lys Val Ala Pro Thr Gln Ser
      195     200     205
Asp Pro Ile Asn Leu Lys Phe Glu Pro Pro Leu Gly Asp Asn Ser Pro
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Leu Leu Ala Ala Arg Ser Lys Ser Ser Ser Gly Gly His Leu Pro Leu
      225     230     235     240
Pro Thr Asn Pro Ser Pro Asp Ser Ala Ile His Ser Val Tyr Thr His
      245     250     255
Ser Ser Pro Ser Gln Ser Pro Leu Thr Ser Arg His Ala Pro Tyr Thr
      260     265     270
Pro Ser Leu Ser Arg Asn Asn Ser Asp Ala Ser His Ser Ser Cys Tyr
      275     280     285
Ser Tyr Ser Ser Glu Phe Ser Pro Thr His Ser Pro Ile Gln Ala Arg
      290     295     300
His Ala Pro Pro Ala Gly Thr Leu Tyr Gly Asn His His Gly Ile Tyr
      305     310     315     320

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Arg Gln Met Lys Val Glu Ala Ser Ser Thr Val Pro Ser Ser Gly Gln
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 Glu Ala Gln Asn Leu Ser Met Asp Ser Ala Ser Ser Asn Leu Asp Thr
 340 345 350
 Val Gly Leu Gly Ser Ser His Pro Ala Ser Pro Ala Gly Ile Ser Arg
 355 360 365
 Gln Gln Leu Ile Asn Ser Pro Cys Pro Ile Cys Gly Asp Lys Ile Ser
 370 375 380
 Gly Phe His Tyr Gly Ile Phe Ser Cys Glu Ser Cys Lys Gly Phe Phe
 385 390 395 400
 Lys Arg Thr Val Gln Asn Arg Lys Asn Tyr Val Cys Val Arg Gly Gly
 405 410 415
 Pro Cys Gln Val Ser Ile Ser Thr Arg Lys Lys Cys Pro Ala Cys Arg
 420 425 430
 Phe Glu Lys Cys Leu Gln Lys Gly Met Lys Leu Glu Ala Ile Arg Glu
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 Asp Arg Thr Arg Gly Gly Arg Ser Thr Tyr Gln Cys Ser Tyr Thr Leu
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 Pro Asn Ser Met Leu Ser Pro Leu Leu Ser Pro Asp Gln Ala Ala Ala
 465 470 475 480
 Ala Ala Ala Ala Ala Ala Val Ala Ser Gln Gln Gln Pro His Gln Arg
 485 490 495
 Leu His Gln Leu Asn Gly Phe Gly Gly Val Pro Ile Pro Cys Ser Thr
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 Ser Leu Pro Ala Ser Pro Ser Leu Ala Gly Thr Ser Val Lys Ser Glu
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 Glu Met Ala Glu Thr Gly Lys Gln Ser Leu Arg Thr Gly Ser Val Pro
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 Pro Leu Leu Gln Glu Ile Met Asp Val Glu His Leu Trp Gln Tyr Thr
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 Asp Ala Glu Leu Ala Arg Ile Asn Gln Pro Leu Ser Ala Phe Ala Ser
 565 570 575
 Gly Ser Ser Ser Ser Ser Ser Ser Ser Gly Thr Ser Ser Gly Ala His
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 Ala Gln Leu Thr Asn Pro Leu Leu Ala Ser Ala Gly Leu Ser Ser Asn
 595 600 605
 Gly Glu Asn Ala Asn Pro Asp Leu Ile Ala His Leu Cys Asn Val Ala
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 Asp His Arg Leu Tyr Lys Ile Val Lys Trp Cys Lys Ser Leu Pro Leu
 625 630 635 640
 Phe Lys Asn Ile Ser Ile Asp Asp Gln Ile Cys Leu Leu Ile Asn Ser
 645 650 655
 Trp Cys Glu Leu Leu Phe Ser Cys Cys Phe Arg Ser Ile Asp Thr
 660 665 670
 Pro Gly Glu Ile Lys Met Ser Gln Gly Arg Lys Ile Thr Leu Ser Gln
 675 680 685
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 690 695 700
 Thr Asp His Leu Arg Arg Leu Arg Val Asp Arg Tyr Glu Tyr Val Ala
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 Met Lys Val Ile Val Leu Leu Gln Ser Asp Thr Thr Glu Leu Gln Glu
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 Leu Leu Leu Arg Ile Pro Asp Leu Gln Arg Thr Cys Gln Leu Gly Lys
 770 775 780
 Glu Met Leu Thr Ile Lys Thr Arg Asp Gly Ala Asp Phe Asn Leu Leu
 785 790 795 800

Met Glu Leu Leu Arg Gly Glu His
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<210> 36

<211> 4841

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 36

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taacaaatct	tatcaacaca	gcaacggaaa	tacattaaaa	tcttgataga	ctgagaaagg		420
gacaattgga	atacttttag	ttatttttta	atgttttaca	acacaatgga	actgcatcaa		480
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<210> 37

<211> 7555

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 37

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<210> 38

<211> 545

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 38

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gttcatgaat	accccagctc	gcccgggtgc	ggggagcagc	ccagtacatt	ctacgtacgg	300
tggatgcaat	ctgaagttca	tcacaacggt	tgacgagaag	tggcgcatgg	acgagaacat	360
aatcctgata	atgtgtgcca	ttgtccttta	atgtctattt	gaatgttaac	ccatcccagg	420
tggagccctt	gctgcgtgaa	atattcgatc	aaagagagca	tatttaggat	accaagtgca	480
aagcaacaca	atctataaga	cgataatgca	ataactaact	tggaagcgtg	ggttctgtgc	540
aaacc						545

<210> 39

<211> 1119

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 39

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<210> 40

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 40

gagagatgtg	cttcgttaaa	gcatcaaccc	30
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<210> 41

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 41
ggactagtag atctagagga ttctacaaat gtccagtgtc tccc 44

<210> 42
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 42
ccattattat cgccataatc gtaaagg 27

<210> 43
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 43
attaccctgt tatccctagc gggttacctt aatgcgatca tcgccc 46

<210> 44
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 44
ggaaagcttt tcctgctgat caataatacc 30

<210> 45
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 45
tgggcccatc acttgcttgt aaccgccgaa gaactgcgcg g 41

<210> 46
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 46
cgctagggat aacagggttaa taacagtcca cggtattagc ctatagg

47

<210> 47
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 47
cgattatggc gataataatg gccaaagaga acatgggcaa catacgc

47

<210> 48
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 48
gaagcaagcc tctagaaaga tgaagc

26

<210> 49
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 49
cgtgccgttc tccatcgata cagtcaactg tctttgacc

39

<210> 50
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 50
gcctggatag tcgatcaaat gcg

23

<210> 51
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 51
atggagaacg gcacggatgc 20

<210> 52
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 52
tacattctag agaccaacta caacgacgag cccagtctgg 40

<210> 53
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 53
cattcatccg gacattaatt atgaacttgt tcagacgctc c 41

<210> 54
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 54
gggcatcaac tccggaatta aatgcccgcac acgcatcgg 39

<210> 55
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 55
gtctcacgac gttttgaacc cagaaatcga gctcgcccg gg 42

<210> 56
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 56

cacgaattcc aaactgtctc acgacgtttt gaaccc

36

<210> 57

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 57

gagagctagc atgccggcta gatctcgaga tcggccggcc tagg

44

<210> 58

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 58

gaactgcagc tcgagagcta gcatgccggc

30

<210> 59

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 59

ggagatatatc atatggctag catgactggt gg

32

<210> 60

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 60

tgctcgaagc ttcgcagaag ataatagtag g

31